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Mary Hale, Information Branch Supervisor
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Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

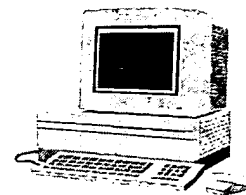
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Search Results

Feedback Form (Optional)



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The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

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➤ *I am an examiner in Workgroup:* (Example: 1610)

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- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, CM1-1E01 or e-mail mary.hale@uspto.gov.

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:47:00 ; Search time 23 Seconds
(without alignments)
1425.297 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1858

Sequence: 1 EFMHHHHHLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	56.6	429	1 EHRT	Ig epsilon chain C
2	940.5	50.6	388	1 EHMS	Ig epsilon chain C
3	871.5	46.9	548	2 S28864	Ig epsilon chain C
4	862.5	46.4	423	1 EHMS	Ig epsilon chain C
5	745	40.1	428	1 EHHU	Ig epsilon chain C
6	741	39.9	426	2 I36948	Ig epsilon chain C
7	587	31.6	572	2 B46529	Ig epsilon chain C
8	560	30.1	504	2 S00390	Ig epsilon chain C
9	499	26.9	627	2 S14683	Ig epsilon chain C
10	490	26.4	479	1 MHRBM	Ig epsilon chain C
11	488.5	26.3	453	2 S37768	Ig epsilon chain C
12	488.5	26.3	474	2 S15590	Ig epsilon chain C
13	488	26.3	458	1 MHRB	Ig epsilon chain C
14	484.5	26.1	391	1 MHHUBT	Ig epsilon chain C
15	477	25.7	452	1 MHHU	Ig epsilon chain C
16	477	25.7	473	1 MHHUM	Ig epsilon chain C
17	469.5	25.3	433	2 S31436	Ig epsilon chain C
18	468	25.2	326	1 MHDG	Ig epsilon chain C
19	464.5	25.0	450	1 MHDG	Ig epsilon chain C
20	464	25.0	328	2 I47161	Ig epsilon chain C
21	461.5	24.8	448	2 S03186	Ig epsilon chain C
22	459.5	24.7	328	2 I47160	Ig epsilon chain C
23	456.5	24.6	328	2 I47159	Ig epsilon chain C
24	455.5	24.5	455	1 MMS	Ig epsilon chain C
25	455.5	24.5	455	2 A24976	Ig epsilon chain C
26	455.5	24.5	476	1 MMSM	Ig epsilon chain C
27	454	24.4	328	2 I47158	Ig epsilon chain C
28	454	24.4	592	2 S25705	Ig epsilon chain C
29	451.5	24.3	327	1 G4HU	Ig epsilon chain C

ALIGNMENTS

RESULT 1

EHRT

Ig epsilon chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999

C:Accession: A93442; A90937; A02143

R:Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.

Nucleic Acids Res. 10, 6041-6049, 1982

A:Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A:Reference number: A93442; MUID:83064537; PMID:6292865

A:Accession: A93442

A:Molecule type: mRNA

A:Residues: 1-429 <HEL>

A:Experimental source: strain LOU/c/Wsl, immunocytoma IR2

R:Kindsvoegel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 335-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, i

A:Reference number: A90937; MUID:83182019; PMID:6820340

A:Contents: myeloma IR162

A:Accession: A90937

A:Molecule type: mRNA

A:Residues: 'N',169-307,'L',309-342 <KIN>

A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin C region: immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:118-80/Domain: immunoglobulin homology <IM1>

F:118-86/Domain: immunoglobulin homology <IM2>

F:223-291/Domain: immunoglobulin homology <IM3>

F:327-398/Domain: immunoglobulin homology <IM4>

F:46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 56.6%; Score 1051; DB 1; Length 429;

Best Local Similarity 62.6%; Pred. No. 3.7e-70;

Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 17 PVTIIPPTVKLFHSCDPRGDAHSTIQLCLVSGSPAKVHVTVLVDGQEAENLFPYTR 76

Db 97 PNIITKPTVDLLHSCDQNA-FHSTIQLYCFYGHQNDVSIHLMDDRKI-----YETH 150

Qy 77 PK----REGGQTFSLQSEVNITQGMSSNTYTCVKINGISFEDSSRRCSDDPRGVIT 132

Db 151 AQNVLIKEEGKLASTYSLRNITQQMMSEFTTCVYQENYWAHTRCSDDEPRGVIT 210

Qy 133 YLIPSPDLVYENGTPKUTCLVLDESEENITVTWVRERKKSIGSASORSTKHHATTSI 192

Db 211 YLIPSPDLVYENGTPKUTCLVLDESEENITVTWVRERKKSIGSASORSTKHHATTSI 270

Qy 193 TSILPVDKADWIEGEGYOCRVDPHFPKPIVRSITKLPGKRLAPEVYMLPPSPETGTR 252

Db 271 TSILPVDKADWIEGEGYOCRVDPHFPKPIVRSITKAPGKSAPEVYVFLPPEEKKDKR 330

Db 128 ILNDVSVLWDDREITDTLAQTVLKBE-GKLASTCSKLNITEQWSESTFTCRVTSQ 186
Qy 112 GSIFEDSSRRCSDDPRGVITYLIPSPDLVYENGTPKLTCLVLDSLEENITVWVER 171
Db 187 GVDYLAHTRRCPCDHEPRGAIYTLIPSPDLVYQNGAPKLTCLVLDSESKNVNVTWQEK 246
Qy 172 KKSIGSASORSTKHH-HATTSTSTLVDADKWIEGEGYQCEVDHPHPKPIVRSITKLP 230
Db 247 KTSV-SASQWYTKHNNATSTSLPVVAKDWIEGYQCVVDRPDPKPIVRSIT-LP 304
Qy 231 --GKRLAPEVYMLPSPBETGTRVTCILIRGFYSEISVQWLPNNEEDHTGHHTTRPQ 288
Db 305 QVSQSAEVEVVPPESESEDKRLTLCIQNFPEDSLQVWLGDKLINSQHSITTPPL 364
Qy 289 KDHGTRDFEFLYSRLMVKNSIWEKNLVTCRVVHVALPGSRRTLEKSLHYSAGN 341
Db 365 KNSGNSQGGFFIPSRLEVAKTLWTKQKPTQCVIHEALQKPRKLEKTIISTSLGN 417
RESULT 5
EHU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence revision 13-Jun-1993 #text change 16-Jul-1999
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R:Flanagan, J.G.; Rabbits, T.H.
EMBO J. 1, 655-660, 1982
A:Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FA>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hiseajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A:Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: GB:J00222; NID:g184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A:Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: EMBL:X63693; GB:S38668; NID:g32987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugl
Nucleic Acids Res. 11, 719-726, 1983
A:Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A:Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: GB:J00222; NID:g184755
A:Note: this sequence difference may be due to polymorphism
R:Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: Protein
A:Residues: 'GAWTL', 6, 'X', 8-16, 'B', 18-43, 'B', 45-52, 55-92, 95-97, 'B', 99-121, 'B', 123, 'L', 12
A:Experimental source: myeloma protein Nd

R:Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A:Title: Cloning and sequence determination of the gene for the human immunoglobulin eps
A:Reference number: A93933; MUID:83065234; PMID:6815656
A:Accession: B93933
A:Molecule type: mRNA
A:Residues: 1-40,68-114,427-428 <KEN>
A:Cross-references: GB:L00022; NID:g185035
R:Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A:Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragmen
A:Reference number: S02438; MUID:88083554; PMID:3121387
A:Accession: S02438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 98-352 <IKE>
R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A:Reference number: A53116; MUID:94103254; PMID:8276835
A:Accession: A53116
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 320-428 <ZH>
A:Experimental source: myeloma U266-derived cell line AP-10
A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R:Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A:Reference number: A46536; MUID:93122085; PMID:8419166
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-426 <HEL>
A:Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125297)
A:Accession: D46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 382-391 <HE2>
A:Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:125299)
A:Accession: A46536
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 401-428 <HE3>
A:Cross-references: GB:S53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A:Experimental source: B cell myeloma U-266
A:Note: sequence extracted from NCBI backbone (NCBIP:123483)
C:Genetics:
A:Gene: GDB:IGHE
A:Cross-references: GDB:119335; OMIM:147180
A:Map position: 14q32.33-14q32.33
A:Introns: 1/1; 104/1; 211/1; 319/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region: immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuli
F:22-87/Domain: immunoglobulin homology <IM1>
F:128-195/Domain: immunoglobulin homology <IM2>
F:232-301/Domain: immunoglobulin homology <IM3>
F:338-407/Domain: immunoglobulin homology <IM4>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:15-105,23-85,135-193,239-299,345-405/Disulfide bonds: #status predicted
F:121,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
Query Match 40.1%; Score 745; DB 1; Length 428;
Best Local Similarity 44.4%; Pred No. 1.5e-47;
Matches 143; Conservative 62; Mismatches 109; Indels 8; Gaps 5;

```
Qy 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLVGQAEANLFPYTTTRPKREG 81
Db 111 PPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTNITWLEDGQVMD--VDLSTASTTQE 168
Qy 82 GQTFSLQSEVNTIQGOWMSSNTYTCVTKHNGSIFEDSSRRCSDDPRGVITYLIPPSPLD 141
Db 169 GELASTQSELTLSQKHLSDRIYTCQVYTGHTFEDSTKCCADSPRGVSAYLSRSPFD 228
Qy 142 LVENGTPTKLTCLVLDL-ESEENITVTVWRERKKSIGSASQSRSTKHHATTSTSLPVD 200
Db 229 LPIKSPITITCLVLDLAPSKGTWNLTSRASGKPNVHSTRKEQKQNGTLTSTLPGVT 288
Qy 201 KDWIEGEGYQCRVDHPHFKPIVRSITKLPKGLAPEVVMPLPSPRETCG--TRTVTCL 258
Db 289 RWIEGETYQCRVTHPLPALMRSTTKSGPRAAPEVYAF-ATPEWPSGRDKRTLACLI 347
Qy 259 RGFPYSEISVQWLPNNEEDHTGHTTTRPKQDGTDPSPFLYRMLVNSKIWEKGNLVT 318
Db 348 QNFMPEDISVQWLNHVEQLPDARHSTTQPRKTKGS--GFFVFSRLVTRAWEQKDEFIC 405
Qy 319 RVVHEALPGSRTEKSLHYSAG 340
Db 406 RAVHEAASPSTQVQRAVSNPG 427
RESULT 6
Ig epsilon-chain - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C:Accession: I36948
R:Sakoyama, Y.; Hong, K.
A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan
A:Reference number: I36948; MUID:87147196; PMID:3103123
A:Accession: I36948
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-426 <RES>
A:Cross-references: GB:M15398; NID:g176797; PIDN:AAA35416.1; PID:g176798
C:Introns: 103/1; 209/1; 317/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:336-405/Domain: immunoglobulin homology <IMM>
Query Match 39.9%; Score 741; DB 2; Length 426;
Best Local Similarity 44.5%; Pred. No. 2.9e-47;
Matches 143; Conservative 60; Mismatches 110; Indels 8; Gaps 5;
Qy 23 PPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHVHTWLVGQAEANLFPYTTTRPKREG 82
Db 110 PPTVKILQSSCDGGHFPPTIQLCLVSGYTGTTNITWLEDGQVMD--VDLSTASTTQE 167
Qy 83 QTFSLQSEVNTIQGOWMSSNTYTCVTKHNGSIFEDSSRRCSDDPRGVITYLIPPSPLD 142
Db 168 ELASTQSELTLSQKHLSDRIYTCQVYTGHTFEDSTKCCADSPRGVSAYLSRSPFD 227
Qy 143 YENGTPTKLTCLVLDL-ESEENITVTVWRERKKSIGSASQSRSTKHHATTSTSLPVD 201
Db 228 FIRKSPITITCLVLDLAPSKGTWNLTSRASGKPNVHSTRKEQKQNGTLTSTLPGVT 287
Qy 202 DWIEGEGYQCRVDHPHFKPIVRSITKLPKGLAPEVVMPLPSPRETCG--TRTVTCLIR 259
Db 288 DWIEGETYQCRVTHPLPALMRSTTKSGPRAAPEVYAF-ATPEWPSGRDKRTLACLI 346
Qy 260 GFVPSISVQWLPNNEEDHTGHTTTRPKQDGTDPSPFLYRMLVNSKIWEKGNLVT 319
Db 347 NFMPEDISVQWLNHVEQLPDARHSTTQPRKTKGS--GFFVFSRLVTRAWEQKDEFIC 404
Qy 320 VVHEALPGSRTEKSLHYSAG 340
Db 405 AVHEAASPSTQVQRAVSNPG 425
```

RESULT 7

B46529

Ig Y heavy chain (7.8S) - duck

N:Alternate names: Ig gamma chain (7.8S)

C:Species: Anas platyrhynchos (domestic duck)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: B46529; S20759

R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.

J. Immunol. 149, 2627-2633, 1992

A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: mo

A:Reference number: A46529; MUID:93017865; PMID:1401901

A:Accession: B46529

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-572 <MAG>

A:Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443

A:Experimental source: spleen

A:Note: sequence extracted from NCBI backbone (NCBIP:116127)

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 31.6%; Score 587; DB 2; Length 572;

Best Local Similarity 37.3%; Pred. No. 9.8e-36;

Matches 121; Conservative 60; Mismatches 129; Indels 14; Gaps 8;

Qy 22 PPTVKLFHSS-CDPRGDAHSTIQLCLVSGSPAKVHVHTWLVGQAEANLFPYTTTRPKRE 80

Db 249 PPEVQLVHSSCTSLGD--DSVELLCVITGFPSPPEVEVWLVGAPA-HLVATMTRPQRE 305

Qy 81 -GGQTFSLQSEVNTIQGOWMSSNTYTCVTKH-NGSIFEDSSRRCSDDPRG--VITYL 134

Db 306 AGSKTYATSTNVSREDWKAGKFTCKVKEPATGCTGTAQGHARFCPGSGAOSCSPIQIFV 365

Qy 135 IPPPLDLVYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQSRSTKHHATTSTITS 194

Db 366 VPPSPGSLYIRQDAKVHCLVNLPSDASLSISWTRKSGALRPDPMLVTEHFNCTFIASS 425

Qy 195 ILPVDADKDWIEGEGYQCRVDHPHFKPIVRSITKLPKGLAPEVVMPLPSPRETCGTTT 253

Db 426 SLAISTQDLAGERFTCTVQHEDLFVPLGKSIAGHAGKVTAPYITFTFPFHAEELSIAEVT 485

Qy 254 VTCLIRGEPYSEISVQWLPNNEEDHTGHTTTRPKQDGTDPSPFLYRMLVNSKIWEKG 313

Db 486 LTCLVRGEPQPEHVEVQWLRNHSVPAAEFVTTPLKEPNGDGTFFLYSKMTVPKASWQGG 545

Qy 314 NLVTCRVVHEALP--GSRTLEKS 334

Db 546 VSYACVWVHEGLPMRFTORPLOKT 569

RESULT 8

S00390

Ig gamma chain (clone 36) - chicken (fragment)

N:Alternate names: Ig nu chain

C:Species: Gallus gallus (Chicken)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000

C:Accession: S00390

R:Parvari, R.; Avivi, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schechter, I.

EMBO J. 7, 739-744, 1988

A:Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combinat

A:Reference number: S00390; MUID:88283642; PMID:3135182

A:Accession: S00390

A:Molecule type: mRNA

A:Residues: 1-504 <PAR>

A:Cross-references: EMBL:X07174

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 30.1%; Score 560; DB 2; Length 504;

Best Local Similarity 35.7%; Pred. No. 8.2e-34;

Matches 119; Conservative 57; Mismatches 137; Indels 20; Gaps 8;

Qy 17 PVTIPTTKVLKFH-SSCDPRGDAHSTIQLCLLVSGFSPAKVHVTLVLDGQEAENLFFPYTT 75
Db 172 PVPVPAPEQVHLHASSCTP--SQSEVELLCVLTGFGSPASAEVWLDG--VGGLLVASQ 227

Qy 76 RPKEGGGTFSLOSBNITQGMSSNTYTCHVKH--NGSTFEDSSRSCD--DEPRGVI 131
Db 228 SPAVRSGSTYLSRRVNVSGTDWREGKYSYCRVHRPATNTVVEDHVKGCPDGAQSCSPIQ 287

Qy 132 TYLPPSPDLVYENGTPKLTCLVLDSEENITVTVWRERKKSIGSASQSRSTKHHHTTS 191
Db 288 LYAIPSPGELYISIDAKRLCVNLPSDDSLSVTWTRKSNLRLPDPMPVLQEHFNCTYS 347

Qy 192 ITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRLEPEVYMLPPSPBEETGT 251
Db 348 ASSAVPVSTQDWLSGERFTCTVQHEELPLPSKSVYRNTGPTTPLLIVPAPHPPELSLS 407

Qy 252 R-TVTCLIRGFPYPSISVQWLPNNEEDHTGHTTTRPOKDH-----GTDPSPFLYSRM 303
Db 408 RVTLSCLVRGFRPRDIEIRWLDRHRAVPATEFVTTTAVLPEERTANGAGGDGDTFFVYSKM 467

Qy 304 LVNKSIEWKGMLNLCRVVHEALP---GSRTEK 333
Db 468 SVETAKWNGTTFACMAVHEALPMRFSORTLOK 500

RESULT 9
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleoside sequence of the membrane form of the human IGM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRI>
A:Cross-references: EMBL:X17115; NID:g33450; PID:CAA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 26.9%; Score 499; DB 2; Length 627;
Best Local Similarity 31.5%; Pred. No. 3.5e-29;
Matches 106; Conservative 72; Mismatches 135; Indels 24; Gaps 9;

Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLLVSGFSPAKVHVTLVLDGQEAEN 69
Db 284 PLPVAELPPKVSVP---VPPRDGFGNPRSKSKLICQATGFSRQIQVSLUREGQVGS 310

Qy 70 LFPYTT-----RPKEGGGTFSLOSBNITQGMSSNTYTCHVXNGSIF-EDSSRCS 123
Db 311 --GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMTCTCRVDHRLGTLTQGNASSMVCV 368

Qy 124 DDEPRGVITYLIPSPDLVYENGTPKLTCLVLDSEENITVTVWRERKKSIGSASQSRST 183
Db 369 PQDQTAIRVAIPSPFASIFLTKSLTCLVLDLTYDSVTISWTRQNGEAVKTHTNISE 428

Qy 184 KHHHTTSITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRLE-APEVYMLP 242
Db 429 SHPNATPFAVNGEASICEDDWSNGERTCTVTTDPLSPKQTSIRPKGVALLHRPDDVLLP 488

Qy 243 PSPEETG--TTRTAVTCLIRGFPYPSISVQWLPNNEEDHTGHTTTRPOKDHGTDPSPFLY 300
Db 489 PAREQLNRESATITCLVTGFGSPADVFVQMQRGQPLSPKEKYTSAPWPEQAPGRYFAH 548

Qy 301 SRMLVNKSIEWKGMLNLCRVVHEALPG---SRTLEKS 334
Db 301 SRMLVNKSIEWKGMLNLCRVVHEALPG---SRTLEKS 334

Db 549 SILTVSEEWNTGTYYTCVVAHEALPNRVTERTVDKS 585

RESULT 10
MHRBM
Ig mu chain C region, membrane-bound form - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 23-Aug-1997
C:Accession: A02165; A02164
R:Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J. Immunol. 132, 490-495, 1984
A:Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a
A:Reference number: A02164; MUID:84088930; PMID:6418803
A:Contents: a2 allotype
A:Accession: A02165
A:Molecule type: mRNA
A:Residues: 439-479 <BE2>
A:Accession: A02164
A:Molecule type: mRNA
A:Residues: 1-438, 'GKPTLVNVLMSDASTCY' <BER>
A:Note: the sequence of residues 1-438 was assumed to be identical with the corresponding
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:21-92/Domain: immunoglobulin homology <IMM1>
F:130-202/Domain: immunoglobulin homology <IMM2>
F:242-310/Domain: immunoglobulin homology <IMM3>
F:349-420/Domain: immunoglobulin homology <IMM4>
F:439-479/Domain: carboxyl-terminal <CTS>
F:14/Disulfide bonds: interchain (to light chain) #status predicted
F:28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted
F:46,114,212,261,277,284/Binding site: carbohydrate (Asn) (covalent)
F:219/Disulfide bonds: interchain (to heavy chain) #status predicted
F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.4%; Score 490; DB 1; Length 479;
Best Local Similarity 32.4%; Pred. No. 1.1e-28;
Matches 114; Conservative 62; Mismatches 158; Indels 18; Gaps 8;

Qy 5 HHHHTLSIPESGPV-TIIPPTVKLFHSSCDP-RGDAHSTIQLCLLVSGFSPAKVHVTLV 62
Db 94 HSNRDLRVSPFVDSLPNNVSFIPPRDSFGSGTKRSKRLICQATGFSRQIQVSLVSR 153

Qy 63 DQQAEN---LFPYTRPRKGGGTFSLOSBNITQGMSSNTYTCHVXNGSIFEDS- 118
Db 154 DQQVESGVLTKPVEATKGAGPATFSSSMLTITESDWLSQSLYTCRVDRHGFDDK 213

Qy 119 --SRCSDDPRGVITYLIPSPDLVYENGTPKLTCLVLDSEENITVTVWRERKKSIG 176
Db 214 SMSSECSSTPSFGIQVFPFIAPSFADTFLSKSARLICLVTDLTLYGSLNLSWASHNGKALD 273

Qy 177 SASQSRSTGHHHTTSITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRLEA- 235
Db 274 THMNTESHNPATFSAMGEASVCAEDWESGQFTCTVTHADLPFLPKHTISK--SREVAK 331

Qy 236 --PEVYMLPPSPES--TGTTRTAVTCLIRGFPYPSISVQWLPNNEEDHTGHTTTRPOKDH 291
Db 332 HPPAVYVLPAREQLVRESATVTVLVKGFSPADVFVQMQRGQPLSSDKYTSAPAPEP 391

Qy 292 GTDPSFFLYSRMLVNKSIEWKGMLNLCRVVHEALP---GSRTEKSLHYSAG 340
Db 392 QAPGLYFTHSTLTVTEDWNSGETFTCVVGEALPHMVMTERTVDKSTGEVG 443

RESULT 11
S37768
Ig mu chain C region - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 23-Jul-1999
C:Accession: S37768
R:Harindranath, N.; Donadel, G.; Sigounas, G.; Notkins, A.L.
Mol. Immunol. 30, 111-112, 1993

[illegible]

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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:47:30 ; Search time 19 Seconds
(without alignments)
528.064 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1858

Sequence: 1 EPHHHHTLSLPESGPVTI.....HEALPGSRITLKSLSHYSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950.5	51.2	426	1 US-08-336-583-2	Sequence 2, Appli
2	950.5	51.2	426	5 PCT-US95-13795-2	Sequence 2, Appli
3	862.5	46.4	561	3 US-09-192-545-2	Sequence 2, Appli
4	507	27.3	331	2 US-08-646-981-17	Sequence 17, Appli
5	493.5	26.6	334	2 US-08-646-981-16	Sequence 16, Appli
6	488	26.3	504	1 US-07-932-915-2	Sequence 2, Appli
7	488	26.3	504	5 PCT-US91-05826-2	Sequence 2, Appli
8	475.5	25.6	333	1 US-08-436-483-6	Sequence 6, Appli
9	475.5	25.6	333	1 US-08-024-253-6	Sequence 6, Appli
10	475	25.6	450	2 US-08-788-800-12	Sequence 12, Appli
11	475	25.6	469	2 US-07-934-373C-23	Sequence 23, Appli
12	475	25.6	469	3 US-08-437-642B-23	Sequence 23, Appli
13	475	25.6	469	4 US-08-146-206C-23	Sequence 23, Appli
14	469.5	25.3	530	3 US-08-477-460B-4	Sequence 4, Appli
15	469.5	25.3	530	3 US-08-379-516-4	Sequence 4, Appli
16	469.5	25.3	530	4 US-08-329-916-4	Sequence 4, Appli
17	469.5	25.3	530	4 US-08-485-372A-4	Sequence 4, Appli
18	469.5	25.3	530	4 US-09-409-006A-4	Sequence 4, Appli
19	469.5	25.3	530	4 US-08-484-681-4	Sequence 4, Appli
20	469.5	25.3	530	5 PCT-US93-07422-4	Sequence 4, Appli
21	457	24.6	326	2 US-08-656-586-9	Sequence 9, Appli
22	454	24.4	552	5 PCT-US93-07832-23	Sequence 23, Appli
23	451.5	24.3	327	2 US-08-761-277A-47	Sequence 47, Appli
24	451.5	24.3	443	5 PCT-US96-13152-4	Sequence 4, Appli
25	451.5	24.3	467	1 US-08-704-744-81	Sequence 81, Appli
26	451.5	24.3	467	4 US-08-523-894-8	Sequence 8, Appli
27	451.5	24.3	467	4 US-08-523-894-10	Sequence 10, Appli

28	451.5	24.3	467	4 US-08-523-894-12	Sequence 12, Appli
29	447	24.1	451	4 US-09-247-352-3	Sequence 3, Appli
30	447	24.1	451	4 US-09-466-635-3	Sequence 3, Appli
31	447	24.1	472	4 US-09-301-593-30	Sequence 30, Appli
32	447	24.1	472	4 US-09-301-593-43	Sequence 43, Appli
33	446.5	24.0	451	2 US-08-887-352B-14	Sequence 14, Appli
34	446.5	24.0	451	2 US-08-887-352B-16	Sequence 16, Appli
35	446.5	24.0	451	2 US-08-887-352B-18	Sequence 18, Appli
36	446.5	24.0	451	3 US-08-466-151-65	Sequence 65, Appli
37	446.5	24.0	451	4 US-09-109-207C-14	Sequence 14, Appli
38	446.5	24.0	451	4 US-09-109-207C-16	Sequence 16, Appli
39	446.5	24.0	451	4 US-09-109-207C-18	Sequence 18, Appli
40	446.5	24.0	451	4 US-09-282-505-2	Sequence 2, Appli
41	446.5	24.0	451	4 US-09-054-255-2	Sequence 2, Appli
42	446.5	24.0	451	4 US-09-296-005-14	Sequence 14, Appli
43	446.5	24.0	451	4 US-09-296-005-16	Sequence 16, Appli
44	446.5	24.0	451	4 US-09-296-005-18	Sequence 18, Appli
45	445.5	24.0	453	3 US-08-466-151-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match 51.2%; Score 950.5; DB 1; Length 426;
Best Local Similarity 53.8%; Pred. No. 2.2e-86;
Matches 175; Conservative 52; Mismatches 95; Indels 3; Gaps 2;

Qy 18 VTIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSKAKVHVTLVDGQAEANLFFVTPRP 77
Sequence 2, Appli

Db 102 INFIPPTVKLFHSSCNPGVDTHTIQLCLISGVPGDMEIWLVDGQKATNFFVTPAG 161
Sequence 8, Appli

Qy 78 KREGGQTFSLQSEVNTIQGQWMSNTYTCVHKHNGSIFEDSSRRCSDDDEPRGVITYLIPP 137
Sequence 10, Appli

Db 162 TKEGNT-STHSELNITQGEWISQKTYTCQVYQGFDFKDEARKCESDPRGVTSYLSPP 220
Qy 138 SPLDLYENGTPKLTCLVLDSEENITVTVRERKKSIGSQRSTKHHATTSTISILP 197
Db 221 SPLDLYVHKAPKITCLVLDATMEGMNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTLP 280
Qy 198 VDAKWIEGEGYQCRVDHPPKPIVRSITKLPKGLAPAEVYMLPPSPETGTTT--TVT 255
Db 281 VNTNDWIEGETYYCRVTHPHLPKDIVRSIAKAPGKRAPPDVVFLFPPPEEQTKDRVLT 340
Qy 198 VDAKWIEGEGYQCRVDHPPKPIVRSITKLPKGLAPAEVYMLPPSPETGTTT--TVT 255
Db 281 VNTNDWIEGETYYCRVTHPHLPKDIVRSIAKAPGKRAPPDVVFLFPPPEEQTKDRVLT 340
Qy 256 CLIRGFYPSSEISVQWLPNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNKS IWEKGNL 315
Db 341 CLIQNFFPADISVQWLRNDSPTQDQYTTTGHKVGSGRPAPFFISRLVSRVDWEQKNK 400
Qy 316 VTCRVVHEALPGSRTLEKSLHYSAG 340
Db 401 FTCQVVEALSGSRILQKWSKTPG 425
RESULT 2
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2
Query Match 51.2%; Score 950.5; DB 5; Length 426;
Best Local Similarity 53.8%; Pred. No. 2.2e-86;
Matches 175; Conservative 52; Mismatches 95; Indels 3; Gaps 2;
Qy 18 VTIIPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVHTWLDGQBAENLFPYVTRP 77
Db 102 LNFIPPTVKLFHSSCNFVGDTHTIQLLCLISGYVFGDMVILWLDGQATNIFPYVAPG 161
Qy 78 KREGGQTFSLQSEVNITQGWSSNTYTCVHKINGSIFEDSSRRCSDDPRGVITVILPP 137
Db 162 TKEGNT-STHSELNITQGEWISQKTYTCQVYQGFDFKDEARKCESDPRGVTSYLSPP 220
Qy 138 SPLDLYENGTPKLTCLVLDSEENITVTVRERKKSIGSQRSTKHHATTSTISILP 197

Db 221 SPLDLYVHKAPKITCLVLDATMEGMNLTWYRESKEPVNPGPLNKKDHFNGTITVTSTLP 280
Qy 198 VDAKWIEGEGYQCRVDHPPKPIVRSITKLPKGLAPAEVYMLPPSPETGTTT--TVT 255
Db 281 VNTNDWIEGETYYCRVTHPHLPKDIVRSIAKAPGKRAPPDVVFLFPPPEEQTKDRVLT 340
Qy 256 CLIRGFYPSSEISVQWLPNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNKS IWEKGNL 315
Db 341 CLIQNFFPADISVQWLRNDSPTQDQYTTTGHKVGSGRPAPFFISRLVSRVDWEQKNK 400
Qy 316 VTCRVVHEALPGSRTLEKSLHYSAG 340
Db 401 FTCQVVEALSGSRILQKWSKTPG 425
RESULT 3
US-09-192-545-2
; Sequence 2, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799P79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: JP HEI 9-313989
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-2
Query Match 46.4%; Score 862.5; DB 3; Length 561;
Best Local Similarity 51.8%; Pred. No. 1.9e-77;
Matches 183; Conservative 46; Mismatches 103; Indels 21; Gaps 8;
Qy 2 FHHHHHTLSLPESGPVTIIPPTVKLFHS-----SCDPRGDAHSTIQLLCLVSGF 51
Db 211 FTCVHTPPSPFNSRRTILVREPT---HSLSPMWSYSIHRCDPNA-PHSTIQLYCFIYGH 265
Qy 52 SPAKVHTWLDVGOBAENLFPYVTRPKREGGQTFSLQSEVNITQGWSSNTYTCVHKHN 111
Db 266 ILNDVSVSWLMDREITDTLAQTVLKEE-GKLASTCCKLNITEQWMSSEFTTCRVTSQ 324
Qy 112 GSIFEDSSRRCSDDPRGVITVILPPSPDLVYENGTPKLTCLVLDSEENITVTVRER 171
Db 325 GVDYLAHTRRCPCDHEPRGAIIVLPPSPDLVYQNGAPKLTCLVLDSEKKNVNTWQEK 384
Qy 172 KKSIGSASQRSTKHH-HATTSTISILPVDADKWIEGEGYQCRVDHPPKPIVRSITKLP 230
Db 385 KTSV-SASQWYTKHHNATTSITILPVVAKDWIEGEGYQCVVDRPDPFKPIVRSIT-LP 442
Qy 231 --GKLAPEVYMLPPSPETGTTTTRVTCILIRGFYPSSEISVQWLPNNEEDHTGHTTTRPQ 288
Db 443 QVSQSAPEVTVFPPEPESEDKRTLTCLIQNFFPEDISVQWLDGKGLINSQHSHTTTP 502
Qy 289 KDHGTDPSFFLYSRMLVNKS IWEKGNLTVTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 503 KNSGNSQGFIFISRLVAKLTWQKQTCQVIEALQKPKLEKTIISTISLGN 555
RESULT 4
US-08-646-981-17
; Sequence 17, Application US/08646981
; Patent No. 5852183

GENERAL INFORMATION:
APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-17

Query Match 27.3%; Score 507; DB 2; Length 331;
Best Local Similarity 35.2%; Pred. No. 2.3e-42;
Matches 118; Conservative 69; Mismatches 122; Indels 26; Gaps 11;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVVDGQEAENLFPYTTTPKREGG 82
Db 5 PSVPFLAPSCG--STSGSTVTLACLIVSGYFPEPVTVSW-NSGSLTSGVHTTTPSVLKSSG- 60

Qy 83 QTFSLQSEVNITQGWMSNTYTCVKNHGS-----IFEDSSRRCSDDPE-----RG 129
Db 61 -LYSLSSMTVPSSR-LPSETFTCNVHVHPATNTKVDKPGVPKESCKICSPCPVESLGG 118

Qy 130 VITYLPPSLDLYE-NGTPKLTCLVLDLESEE-NITVTWVRERKKSIGSASQSRSTKHH 187
Db 119 PSVFIFPPFKDLIRITPEVTCVVLDGREDPEVQISWFVDGKEVITAKTPREQQFN 178

Qy 188 ATTSITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGKRLAPEVYMLPPSP 247
Db 179 STYRVSVLPVIEHQDLWLTGKEFKCRVNHIGLPSPIERTISKARGQAHQPGVVLPPSPKE 238

Qy 248 --TGTTRVTCCLIRGFPSEISVQVLPNNEEDHTGHTTTTPQKHGTDPSFFLYSRMLV 305
Db 239 LSSSDTVTLTCLIKDFPPEIDVEWQSGQPEPESEKYHTTAPQLDE--DGSYFLYSLV 296

Qy 306 NKSIWKNLVTCTRVVHEALPGSRRTLEKSLHYSAG 340
Db 297 DKSRWEQGDPTFCVAVHEALQNHYT-DLSLSHSPG 330

RESULT 5
US-08-646-981-16
; Sequence 16, Application US/08646981
; Patent No. 5852183
; GENERAL INFORMATION:
; APPLICANT: Soulliou, Jean-Paul

APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-16

Query Match 26.6%; Score 493.5; DB 2; Length 334;
Best Local Similarity 33.9%; Pred. No. 5.3e-41;
Matches 116; Conservative 68; Mismatches 121; Indels 37; Gaps 11;

Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTLVVDGQEAENLFPYTTTPK 78
Db 5 PSVPFLAPSCG--STSGSTVTLACLIVSGYFPEPVTVSWNSGSLTSG-----VHTFSD 55

Qy 79 REGQTSLOSEVNITQGWMSNTYTCVKNHGS---IFEDSSRRCSDDPE----- 128
Db 56 LQSSGLYSLSSMTVPSSRW-SSETFTCNVAVHASKTKVDKVPKREGRVPRPPDCPKC 114

Qy 129 -----GVITYLPPSPDL-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGSAS 179
Db 115 PAPMLGSPSVFIPEPKPKDTLLIARTPEVTCVVLDGPEDEVEQISWFDGKQMTAKT 174

Qy 180 QRSTKHHHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGKRLAPEVY 239
Db 175 QPREQFNGTVRVVSVLPVIGHQDLWLTGKGFCTCKVNNKALPSPIERTISKARGQAHQPSVY 234

Qy 240 MLPPSPPE-TGTTTTCVTCCLIRGFPSEISVQVLPNNEEDHTGHTTTTPQKHGTDPSFF 298
Db 235 VLPPSELSNTVSLTCLIKDFPPEIDVEWQSGQPEPESEKYRTTTPQLDE--DGSYF 292

Qy 299 LYSRLVKNKSIWKNLVTCTRVVHEALPGSRRTLEKSLHYSAG 340
Db 293 LYSKLSVDKSRWQGDPTFCVAVHEALQNHYT-QKSLSHSPG 333

RESULT 6
US-07-932-915-2
; Sequence 2, Application US/07932915
; Patent No. 5672486
; GENERAL INFORMATION:
; APPLICANT: Soulliou, Jean-Paul

;; TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
;; TITLE OF INVENTION: Core
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;; STREET: 5 Palo Alto Square, Suite 400
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/932,915
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/646,875
;; FILING DATE: 28-JAN-1991
;; APPLICATION NUMBER: US 07/575,394
;; FILING DATE: 23-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland Ph.D., Bertram I.
;; REGISTRATION NUMBER: 20,015
;; REFERENCE/DOCKET NUMBER: ATLA-001/0105
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-494-7622
;; TELEFAX: 415-857-0663
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 504 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-07-932-915-2

Query Match 26.3%; Score 488; DB 1; Length 504;
Best Local Similarity 31.2%; Pred. No. 3.5e-40;
Matches 103; Conservative 72; Mismatches 133; Indels 22; Gaps 9;
Qy 21 IPPTVKLFHSSCDPR----GDAHSTIQLCLVSGSPAKVHVTVLWDGQEAENLPFYTT- 75
Db 160 LPPKVSVF---VPRDGFNGPRKS-KLICQATGSPRQIQVSWLRGKQVGS--GVTTD 213
Qy 76 ----RPRKGGQTFSLQSEVNITQGMSSNTYTVCHVKGHSIF-EDSSRRCSDDPRGV 130
Db 214 QVQAEAKESGPTYKYVTSITLIKESDMSQSMFTCRVDHRLGTLFQNASMCMVDPQDTAI 273
Qy 131 IYLIPPSPDLVYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQSTKHHATT 190
Db 274 RVFAIPSPSPASIFLTKSTKLTCLVTLDTYDSVTISWTQNGEAVKTHNISHPNATF 333
Qy 191 SITSLPVDADKWIEGEGYQCVDPHPKPIVRSITKLPKRL-APEVYMLPPSPPEETG 249
Db 334 SAVGEASICEDDWSNGERFTCTVHTDLPSPKQIISRPGKVALHRPVDYLLPPAREQLN 393
Qy 250 --TTRVTCLIRGFVPSISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNK 307
Db 394 LRESATITCLTVGSPADVFVQWMQSGQLSPKQIISRPGKVALHRPVDYLLPPAREQLN 393
Qy 308 SIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 454 EEWNTGETYTCVVAHEALPNRVRTVDKS 483

RESULT 7
PCT-US91-05826-2
; Sequence 2, Application PC/TUS9105826
; GENERAL INFORMATION:
; APPLICANT: Soullillon, Jean-Paul

;; TITLE OF INVENTION: Protein Polyligands Joined To A Stable Protein
;; TITLE OF INVENTION: Core
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Bertram I. Rowland, Ph.D.
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/05826
;; FILING DATE: 19910822
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/575,394
;; FILING DATE: 29-AUG-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland Ph.D., Bertram I.
;; REGISTRATION NUMBER: 20,015
;; REFERENCE/DOCKET NUMBER: PF55352-1/BIR
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-494-8771
;; TELEFAX: 415-494-8771
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 504 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US91-05826-2

Query Match 26.3%; Score 488; DB 5; Length 504;
Best Local Similarity 31.2%; Pred. No. 3.5e-40;
Matches 103; Conservative 72; Mismatches 133; Indels 22; Gaps 9;
Qy 21 IPPTVKLFHSSCDPR----GDAHSTIQLCLVSGSPAKVHVTVLWDGQEAENLPFYTT- 75
Db 160 LPPKVSVF---VPRDGFNGPRKS-KLICQATGSPRQIQVSWLRGKQVGS--GVTTD 213
Qy 76 ----RPRKGGQTFSLQSEVNITQGMSSNTYTVCHVKGHSIF-EDSSRRCSDDPRGV 130
Db 214 QVQAEAKESGPTYKYVTSITLIKESDMSQSMFTCRVDHRLGTLFQNASMCMVDPQDTAI 273
Qy 131 IYLIPPSPDLVYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQSTKHHATT 190
Db 274 RVFAIPSPSPASIFLTKSTKLTCLVTLDTYDSVTISWTQNGEAVKTHNISHPNATF 333
Qy 191 SITSLPVDADKWIEGEGYQCVDPHPKPIVRSITKLPKRL-APEVYMLPPSPPEETG 249
Db 334 SAVGEASICEDDWSNGERFTCTVHTDLPSPKQIISRPGKVALHRPVDYLLPPAREQLN 393
Qy 250 --TTRVTCLIRGFVPSISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNK 307
Db 394 LRESATITCLTVGSPADVFVQWMQSGQLSPKQIISRPGKVALHRPVDYLLPPAREQLN 393
Qy 308 SIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 454 EEWNTGETYTCVVAHEALPNRVRTVDKS 483

RESULT 8
US-08-436-463-6
; Sequence 6, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki

* APPLICANT: NISHIYAMA, Kiyoto
* APPLICANT: TOKIYOSHI, Sachio
* TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT
* TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY
* NUMBER OF SEQUENCES: 21
* CORRESPONDENCE ADDRESS:
* ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
* STREET: 419 Seventh Street, N.W., Suite 400
* CITY: Washington
* STATE: D.C.
* COUNTRY: USA
* ZIP: 20004
* COMPUTER READABLE FORM:
* MEDIUM TYPE: Floppy disk
* COMPUTER: IBM PC compatible
* OPERATING SYSTEM: PC-DOS/MS-DOS
* SOFTWARE: Patent In Release #1.0, Version #1.30
* CURRENT APPLICATION DATA:
* APPLICATION NUMBER: US/08/436,463
* FILING DATE: 26-JUN-1995
* CLASSIFICATION: 536
* PRIOR APPLICATION DATA:
* APPLICATION NUMBER: JP 341255/1992
* FILING DATE: 28-NOV-1992
* ATTORNEY/AGENT INFORMATION:
* NAME: YUN, Allen C.
* REGISTRATION NUMBER: 37,971
* REFERENCE/DOCKET NUMBER: KIMACHI=1
* TELECOMMUNICATION INFORMATION:
* TELEPHONE: 202-628-5197
* TELEFAX: 202-737-3528
* INFORMATION FOR SEQ ID NO: 6:
* SEQUENCE CHARACTERISTICS:
* LENGTH: 333 amino acids
* TYPE: amino acid
* TOPOLOGY: linear
* MOLECULE TYPE: protein
* US-08-436-463-6
Query Match 25.6%; Score 475.5; DB 1; Length 333;
Best Local Similarity 32.7%; Pred. No. 3.3e-39;
Matches 112; Conservative 72; Mismatches 121; Indels 37; Gaps 12;
Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLLVGSFSPAKVHVTVW----LVDGQBAENLFPVYTRPK 78
Db 4 PSVFPPLAPSCGTTSGA--TVALACLVLGYFPPEPTVSMNSGALTSG---VHTFPAVL--- 55
Qy 79 REGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFE-DSSRRCSDDP----- 127
Db 56 -QASGLYSLSMVTPSSRWL--SDTFTCNVAHPPTNKVKDTRKTDHPGPKPCDCPKC 113
Qy 128 -----RGVITVLIPLPPSLD-LYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 179
Db 114 PPPEMLGSPSIFPPKPKDTLSISRTPEVTCVLDVLDGPDSDVQITWFDVNTQVYTAKT 173
Qy 180 QRSTKHHHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 174 SPREEQFNSTVRVSVLPILHQDLKGEKFKVNSKSLPSPIERTISKAKQPHEPQVY 233
Qy 240 MLPSPSETGTTR-TVTCLIRGFYPSISVQWLPNNEEDHTGHHTTTPKQKHGTDPSFF 298
Db 234 VLPPAQEELSRLNKSVTCLIKSFHPDIAVEWITGOPEPENNYRTTTPOLD--SDGTTF 291
Qy 299 LYSRLVNKSIWEKGNLVTCTRVVHEALPGSRTEKSLHYSAG 340
Db 292 VYSKLSVDRSHWQRNGNTYTCVSHEALSHHT-KQSLTQSPG 332
RESULT 9
US-08-024-253-6
; Sequence 6, Application US/08024253
; Patent No. 5785968
; GENERAL INFORMATION:

* APPLICANT: KIMACHI, Kazuhiko
* APPLICANT: MAEDA, Hiroaki
* APPLICANT: NISHIYAMA, Kiyoto
* APPLICANT: TOKIYOSHI, Sachio
* APPLICANT: TOHYA, Yukinobu
* APPLICANT: MIKAMI, Takeehi
* TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
* TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
* NUMBER OF SEQUENCES: 23
* CORRESPONDENCE ADDRESS:
* ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
* STREET: 1233 20th Street, N.W., Suite 300
* CITY: Washington
* STATE: D.C.
* COUNTRY: U.S.A.
* ZIP: 20036-8218
* COMPUTER READABLE FORM:
* MEDIUM TYPE: Floppy disk
* COMPUTER: IBM PC compatible
* OPERATING SYSTEM: PC-DOS/MS-DOS
* SOFTWARE: Patent In Release #1.0, Version #1.25
* CURRENT APPLICATION DATA:
* APPLICATION NUMBER: US/08/024,253
* FILING DATE: 19930301
* CLASSIFICATION: 424
* PRIOR APPLICATION DATA:
* APPLICATION NUMBER: JP 79189/1992
* FILING DATE: 28-FEB-1992
* ATTORNEY/AGENT INFORMATION:
* NAME: CANTOR, Herbert I.
* REGISTRATION NUMBER: 24,392
* REFERENCE/DOCKET NUMBER: P-500-23744
* TELECOMMUNICATION INFORMATION:
* TELEPHONE: (202) 887-0400
* TELEFAX: (202) 835-0605
* TELEX: 440706 WEGBR
* INFORMATION FOR SEQ ID NO: 6:
* SEQUENCE CHARACTERISTICS:
* LENGTH: 333 amino acids
* TYPE: amino acid
* TOPOLOGY: linear
* MOLECULE TYPE: protein
* US-08-024-253-6
Query Match 25.6%; Score 475.5; DB 1; Length 333;
Best Local Similarity 32.7%; Pred. No. 3.3e-39;
Matches 112; Conservative 72; Mismatches 121; Indels 37; Gaps 12;
Qy 23 PTVKLFHSSCDPRGDAHSTIQLCLLVGSFSPAKVHVTVW----LVDGQBAENLFPVYTRPK 78
Db 4 PSVFPPLAPSCGTTSGA--TVALACLVLGYFPPEPTVSMNSGALTSG---VHTFPAVL--- 55
Qy 79 REGGQTFSLQSEVNITQGMSSNTYTCHVKHNGSIFE-DSSRRCSDDP----- 127
Db 56 -QASGLYSLSMVTPSSRWL--SDTFTCNVAHPPTNKVKDTRKTDHPGPKPCDCPKC 113
Qy 128 -----RGVITVLIPLPPSLD-LYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 179
Db 114 PPPEMLGSPSIFPPKPKDTLSISRTPEVTCVLDVLDGPDSDVQITWFDVNTQVYTAKT 173
Qy 180 QRSTKHHHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
Db 174 SPREEQFNSTVRVSVLPILHQDLKGEKFKVNSKSLPSPIERTISKAKQPHEPQVY 233
Qy 240 MLPSPSETGTTR-TVTCLIRGFYPSISVQWLPNNEEDHTGHHTTTPKQKHGTDPSFF 298
Db 234 VLPPAQEELSRLNKSVTCLIKSFHPDIAVEWITGOPEPENNYRTTTPOLD--SDGTTF 291
Qy 299 LYSRLVNKSIWEKGNLVTCTRVVHEALPGSRTEKSLHYSAG 340
Db 292 VYSKLSVDRSHWQRNGNTYTCVSHEALSHHT-KQSLTQSPG 332

RESULT 10
US-08-788-800-12
; Sequence 12, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 450 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-788-800-12

Query Match 25.6%; Score 475; DB 2; Length 450;
Best Local Similarity 34.7%; Pred No. 5.8e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTITQLLCLVSGFSPAKVHVWTW----LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
Db 140 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG--VHTFPAVL---QSSGLYSLSSV 192
Qy 91 VNITQGMMSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 193 VVTSSNF--GTQTYTCNVDPKPSNTKVDKTVVERKCCVCPAPPPVAGPSVFLFPKPK 251
Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVERKKSIGASQSTKHHHATTSITSLPV 198
Db 252 DTLMSIRTEVTCVVDVSHEDPEQFNWYDGMVHNKATPREEQFNSTFRVSVLTV 311
Qy 199 DAKWIEGEGYQCRVDHPHFKPIVRSITKLPKRLAPEVYMLPPSPPE-TGTTTRVTCL 257
Db 312 VHQDMLNGKEYCKVSNKGLPAPIEKTISKTKGPQPREQVYTLPPSREEMTKNQVSLTCL 371
Qy 258 IRGFYPSISVQWLPNNEEDHTGHTTTPQKDHGTDSPFFLYSRMLVKNYSIWEKGNLTV 317
Db 372 VKGFYPSDIAVWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 427
Qy 318 CRVVEALPGSRITLKSILHSYAG 340
Db 428 CSVMHEALNHHT-QKSLSLSPG 449

RESULT 11
US-07-934-373C-23
; Sequence 23, Application US/07934373C

; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-23

Query Match 25.6%; Score 475; DB 2; Length 469;
Best Local Similarity 34.7%; Pred No. 6.2e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTITQLLCLVSGFSPAKVHVWTW----LVDGQEAENLFPYTRPKREGGQTFSLQSE 90
Db 159 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG--VHTFPAVL---QSSGLYSLSSV 211
Qy 91 VNITQGMMSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 212 VVTSSNF--GTQTYTCNVDPKPSNTKVDKTVVERKCCVCPAPPPVAGPSVFLFPKPK 270
Qy 141 D-LYENGTPKLTCLVLDLESEE-NITVTWVERKKSIGASQSTKHHHATTSITSLPV 198
Db 271 DTLMSIRTEVTCVVDVSHEDPEQFNWYDGMVHNKATPREEQFNSTFRVSVLTV 330
Qy 199 DAKWIEGEGYQCRVDHPHFKPIVRSITKLPKRLAPEVYMLPPSPPE-TGTTTRVTCL 257
Db 331 VHQDMLNGKEYCKVSNKGLPAPIEKTISKTKGPQPREQVYTLPPSREEMTKNQVSLTCL 390
Qy 258 IRGFYPSISVQWLPNNEEDHTGHTTTPQKDHGTDSPFFLYSRMLVKNYSIWEKGNLTV 317
Db 391 VKGFYPSDIAVWESNGQPEN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 446
Qy 318 CRVVEALPGSRITLKSILHSYAG 340
Db 447 CSVMHEALNHHT-QKSLSLSPG 468

RESULT 12
US-08-437-642B-23

; Sequence 23, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-23

Query Match 25.6%; Score 475; DB 3; Length 469;
Best Local Similarity 34.7%; Pred. No. 6.2e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTIQLCLVSGFSPAKVHVW---LVDGQEAENLFPYTRPKREGQTSLOSE 90
Db 159 RSTSESTAALGCLVKDYPPEPVTVSWNGALTSG---VHTPPAVL-----QSSGLYSLSSV 211
Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 212 VVTSSNP-GTQTYTCNVVDHKPSNTKVDKTVKRCVCEPCPCPAPVAGPSVFLFPKPK 270
Qy 141 D-LYENGTPKLTCLVLDLESE-NITVTWVRERKKSIGASQRTKHHHATTSITSLPV 198
Db 271 DTLMSRTPETCVVVDVSHEDPEVQFNWYDGMVEVHNAKTPREEQFNSTFRVVSULTV 330
Qy 199 DAKDWIEGEGYQCRVDHHPFKPIVRSITKLPGKRLAPEVYMLPSPPE-TGTTTRVTCL 257
Db 331 VHQDWLNGKEYCKVSKNGLPAPIEKTISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 390
Qy 258 IRGFYPSISVQWLPNNEDHTGHTTTRPQKDHGTDPDSFFLYSRLVKNKSIWEKGNLVT 317
Db 391 VKGFYPSDIAVEWESNGQPN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 446

Qy 318 CRVVEALPGSRTLEKSLHYSAG 340
Db 447 CSVMHEALHNYT-QKSLSPG 468
RESULT 13
US-08-146-206C-23
; Sequence 23, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-23

Query Match 25.6%; Score 475; DB 4; Length 469;
Best Local Similarity 34.7%; Pred. No. 6.2e-39;
Matches 112; Conservative 66; Mismatches 115; Indels 30; Gaps 12;
Qy 35 RGDASTIQLCLVSGFSPAKVHVW---LVDGQEAENLFPYTRPKREGQTSLOSE 90
Db 159 RSTSESTAALGCLVKDYPPEPVTVSWNGALTSG---VHTPPAVL-----QSSGLYSLSSV 211
Qy 91 VNITQGMSSNTYTCVHKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 212 VVTSSNP-GTQTYTCNVVDHKPSNTKVDKTVKRCVCEPCPCPAPVAGPSVFLFPKPK 270
Qy 141 D-LYENGTPKLTCLVLDLESE-NITVTWVRERKKSIGASQRTKHHHATTSITSLPV 198
Db 271 DTLMSRTPETCVVVDVSHEDPEVQFNWYDGMVEVHNAKTPREEQFNSTFRVVSULTV 330
Qy 199 DAKDWIEGEGYQCRVDHHPFKPIVRSITKLPGKRLAPEVYMLPSPPE-TGTTTRVTCL 257
Db 331 VHQDWLNGKEYCKVSKNGLPAPIEKTISKTKGQPREQVYTLPPSREEMTKNQVSLTCL 390
Qy 258 IRGFYPSISVQWLPNNEDHTGHTTTRPQKDHGTDPDSFFLYSRLVKNKSIWEKGNLVT 317
Db 391 VKGFYPSDIAVEWESNGQPN--NYKTTTPMLD--SDGSFFLYSKLTVDKSRWQGNVFS 446
Qy 318 CRVVEALPGSRTLEKSLHYSAG 340

Db 447 CSVMEALHNHYT-QKSLSLSPG 468

RESULT 14

US-08-477-460B-4

; Sequence 4, Application US/08477460B

; Patent No. 6034223

; GENERAL INFORMATION:

; APPLICANT: Progenics Pharmaceuticals, Inc.

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,460B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/927,931

; FILING DATE: 07-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 977-9809

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 530 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: homo sapien

; CELL TYPE: lymphocyte

US-08-477-460B-4

Query Match 25.3%; Score 469.5; DB 3; Length 530;

Best Local Similarity 32.8%; Pred. No. 2.6e-38;

Matches 121; Conservative 68; Mismatches 129; Indels 51; Gaps 14;

Qy 10 LSLPESGPVTI-----IPPTVKLFHSSCDP-----RGDAHTIQLLCIV 48

Db 174 LELQDSGTWCTVLQNKQKVFEDIVLAFATKGPSVFLPAPCSRSTSESTAALGCLV 233

Qy 49 SGFSPAKVHTW----LVDQGEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTY 104

Db 234 KDYPFEPVTVSNNGALTSG---VHTFPAVL-----QSSGLYSLSSVVTVPPSSNF-GTQTY 285

Qy 105 TCHVKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPLD-LYENGTPKLTCL 153

Db 286 TCNVDPKPSNTKVDKTVKCCVCEPCPPAPVAGSVFLFPKPKDTLMISRTPEVTCV 345

Qy 154 VLDLESEE-NITVTWVRERKKSIGSASQSRSTKHHHTTSITSLPVDADKDMIEGEGYQCR 212

Db 346 VVDVSHEDPEVQFNWYVDGVEVHNAKTPREBEQFNSTFRVWSVLTVVHQDMLNGKEYCK 405

Qy 213 VDPHPKPIVRSITKLPCKRLAPEVYMLPPSPPEE-TGTRTVTCLIRGFYPSSEISVOWL 271

Db 406 VSNKGLPAPIEKTISKTKGQPREPQVVTLPSPREMTKNQVSLTCLVKGFYPSDIAVEWE 465

Qy 272 PNNEEDHTGHTTTRPQKHGTDPSFFLYSRMLNKSWEKGNLVTGRVVEHALPGSRTL 331

Db 466 SNGQPEN--NYKTTTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYT- 520

Qy 332 EKSLHYSAG 340

Db 521 QKSLSLSPG 529

RESULT 15

US-08-379-516-4

; Sequence 4, Application US/08379516

; Patent No. 6083478

; GENERAL INFORMATION:

; APPLICANT: Allaway, Graham P.

; APPLICANT: Maddon, Paul J.

; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2

; TITLE OF INVENTION: Immunoconjugates and Uses Thereof

; FILE REFERENCE: 41215-A-PCT-US

; CURRENT APPLICATION NUMBER: US/08/379,516

; OPERATING FILING DATE: 1996-06-10

; EARLIER APPLICATION NUMBER: PCT/US93/07422

; EARLIER FILING DATE: 1993-08-06

; EARLIER APPLICATION NUMBER: 07/927,931

; EARLIER FILING DATE: 1992-08-07

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 4

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-379-516-4

Query Match 25.3%; Score 469.5; DB 3; Length 530;

Best Local Similarity 32.8%; Pred. No. 2.6e-38;

Matches 121; Conservative 68; Mismatches 129; Indels 51; Gaps 14;

Qy 10 LSLPESGPVTI-----IPPTVKLFHSSCDP-----RGDAHTIQLLCIV 48

Db 174 LELQDSGTWCTVLQNKQKVFEDIVLAFATKGPSVFLPAPCSRSTSESTAALGCLV 233

Qy 49 SGFSPAKVHTW----LVDQGEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTY 104

Db 234 KDYPFEPVTVSNNGALTSG---VHTFPAVL-----QSSGLYSLSSVVTVPPSSNF-GTQTY 285

Qy 105 TCHVKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPLD-LYENGTPKLTCL 153

Db 286 TCNVDPKPSNTKVDKTVKCCVCEPCPPAPVAGSVFLFPKPKDTLMISRTPEVTCV 345

Qy 154 VLDLESEE-NITVTWVRERKKSIGSASQSRSTKHHHTTSITSLPVDADKDMIEGEGYQCR 212

Db 346 VVDVSHEDPEVQFNWYVDGVEVHNAKTPREBEQFNSTFRVWSVLTVVHQDMLNGKEYCK 405

Qy 213 VDPHPKPIVRSITKLPCKRLAPEVYMLPPSPPEE-TGTRTVTCLIRGFYPSSEISVOWL 271

Db 406 VSNKGLPAPIEKTISKTKGQPREPQVVTLPSPREMTKNQVSLTCLVKGFYPSDIAVEWE 465

Qy 272 PNNEEDHTGHTTTRPQKHGTDPSFFLYSRMLNKSWEKGNLVTGRVVEHALPGSRTL 331

Db 466 SNGQPEN--NYKTTTPPMLD--SDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYT- 520

Qy 332 EKSLHYSAG 340

Db 521 QKSLSLSPG 529

Search completed: March 8, 2003, 07:50:33

Job time : 21 secs

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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:49:30 ; Search time 17 Seconds
(without alignments)
845.884 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1858

Sequence: 1 EPHHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	100.0	341	9	US-10-176-664-4
2	1858	100.0	341	10	US-09-401-636-4
3	1840	99.0	341	9	US-10-176-664-9
4	1840	99.0	341	10	US-09-401-636-9
5	1720	92.6	341	9	US-10-176-664-6
6	1720	92.6	341	10	US-09-401-636-6
7	1691.5	91.0	342	9	US-10-176-664-5
8	1691.5	91.0	342	10	US-09-401-636-5
9	1595	85.8	341	9	US-10-176-664-11
10	1595	85.8	341	10	US-09-401-636-11
11	1555	83.7	345	9	US-10-176-664-10
12	1555	83.7	345	10	US-09-401-636-10
13	1553.5	83.6	342	9	US-10-176-664-8
14	1553.5	83.6	342	10	US-09-401-636-8
15	1529	82.3	341	9	US-10-176-664-3
16	1529	82.3	341	10	US-09-401-636-3
17	1051	56.6	340	9	US-10-176-664-2
18	1051	56.6	340	10	US-09-401-636-2
19	1025	55.2	343	9	US-10-176-664-7

20	1025	55.2	343	10	US-09-401-636-7	Sequence 7, Appli
21	940.5	50.6	421	9	US-09-949-375A-28	Sequence 28, Appl
22	936	50.4	332	9	US-09-949-375A-23	Sequence 23, Appl
23	936	50.4	332	9	US-09-949-375A-25	Sequence 25, Appl
24	936	50.4	332	9	US-09-949-375A-27	Sequence 27, Appl
25	931.5	50.1	431	9	US-09-479-614-14	Sequence 14, Appl
26	931.5	50.1	496	9	US-09-479-614-2	Sequence 2, Appli
27	931.5	50.1	496	9	US-09-479-614-29	Sequence 29, Appl
28	929.5	50.0	432	9	US-09-949-375A-19	Sequence 19, Appl
29	925	49.8	343	9	US-09-949-375A-20	Sequence 20, Appl
30	925	49.8	343	9	US-09-949-375A-22	Sequence 22, Appl
31	745	40.1	323	9	US-09-949-375A-2	Sequence 2, Appli
32	745	40.1	323	9	US-09-949-375A-4	Sequence 4, Appli
33	745	40.1	323	9	US-09-949-375A-6	Sequence 6, Appli
34	745	40.1	331	9	US-10-176-664-1	Sequence 1, Appli
35	745	40.1	331	10	US-09-401-636-1	Sequence 1, Appli
36	745	40.1	428	9	US-10-047-542-60	Sequence 60, Appl
37	745	40.1	428	9	US-09-949-375A-1	Sequence 1, Appli
38	745	40.1	428	10	US-09-316-230-1	Sequence 1, Appli
39	745	40.1	574	9	US-10-047-542-45	Sequence 45, Appl
40	743	40.0	330	9	US-09-949-375A-10	Sequence 10, Appl
41	741	39.9	336	9	US-09-949-375A-8	Sequence 8, Appli
42	741	39.9	441	9	US-09-949-375A-7	Sequence 7, Appli
43	526	28.3	352	9	US-09-828-995B-38	Sequence 38, Appl
44	525	28.3	470	9	US-09-828-995B-11	Sequence 11, Appl
45	520.5	28.0	468	9	US-09-828-995B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-10-176-664-4
; Sequence 4, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-4

Query Match	100.0%	Score	1858;	DB	9;	Length	341;
Best Local Similarity	100.0%	Pred. No.	2e-122;				
Matches	341;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	EPHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60				
Db	1	EPHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW	60				
Qy	61	LVDGQAEHLPPYTRPKREGQOTFSLOEVNITGQWMSNTYTCHVKHNGSIFEDSSR	120				
Db	61	LVDGQAEHLPPYTRPKREGQOTFSLOEVNITGQWMSNTYTCHVKHNGSIFEDSSR	120				
Qy	121	RCSDDPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTWVRKKKSIGSAQ	180				
Db	121	RCSDDPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTWVRKKKSIGSAQ	180				
Qy	181	RSTKHHHTTSITSLPVDADKWISGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM	240				
Db	181	RSTKHHHTTSITSLPVDADKWISGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM	240				

Db 181 RSTKHHATTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM 240
Qy 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Db 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341

RESULT 2

US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match 100.0%; Score 1858; DB 10; Length 341;
Best Local Similarity 100.0%; Pred. No. 2e-122;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVYM 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVYM 60
Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLIPSPDLIYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLIPSPDLIYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Qy 181 RSTKHHATTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM 240
Db 181 RSTKHHATTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM 240
Qy 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Db 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341

RESULT 3

US-10-176-664-9
; Sequence 9, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636

; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-9

Query Match 99.0%; Score 1840; DB 9; Length 341;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVYM 60
Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLIPSPDLIYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLIPSPDLIYENGTPKLTCLVLDLESEENITVTVRERKKSIGSASQ 180
Qy 181 RSTKHHATTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM 240
Db 181 RSTKHHATTSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVYM 240
Qy 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Db 241 LPPSPETGTTTCTVCLIRGFYPSSEISVQWLPNNEDHTGHTTTRPQKHGTDPSPFLY 300
Qy 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTEKSLHYSAGN 341

RESULT 4

US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match 99.0%; Score 1840; DB 10; Length 341;
Best Local Similarity 99.4%; Pred. No. 3.6e-121;
Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVYM 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVYM 60
Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGWSSNTYTCHVKHNGSIFEDSSR 120

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Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Qy 181 RSTKHHATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 240
Db 181 RSTKHHATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 240
Qy 241 LPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 300
Db 241 LPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 5
US-10-176-664-6
; Sequence 6, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-6
Query Match 92.6%; Score 1720; DB 9; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Db 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 179
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 WYTKHHNATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Db 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 7
US-10-176-664-5
; Sequence 5, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-5
Query Match 92.6%; Score 1720; DB 9; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Db 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 179
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 WYTKHHNATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Db 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
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RESULT 6
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6
Query Match 92.6%; Score 1720; DB 10; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Db 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 179
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 WYTKHHNATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Db 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 7
US-10-176-664-5
; Sequence 5, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-5
Query Match 92.6%; Score 1720; DB 10; Length 341;
Best Local Similarity 93.3%; Pred. No. 8.3e-113;
Matches 319; Conservative 9; Mismatches 12; Indels 2; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Db 61 LVDGOEAEALPPTTRPKREGGQTSFLOSEVNITQGMSSNTYTCVKNHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 179
Qy 181 RSTKHH-HATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Db 181 WYTKHHNATTSTISILPVDADKWIIEGEGYQCRVDHPHFKPIVRSITKLPGRKLAPEVY 239
Qy 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Db 240 MLPPSPETGTTTRVTCCLIRGYPSEISVQWLPNNEEDHTGHHTTRPKDHGTDPSPFL 299
Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
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US-10-176-664-5

Query Match 91.0%; Score 1691.5; DB 9; Length 342;
Best Local Similarity 90.9%; Pred. No. 8.1e-111;
Matches 311; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSARS 180
Qy 181 RSTK-HHHATTTSITLPPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPCKRLAPEVY 239
Db 181 LVVKEQYNGTFTVSHLPVNTDWDIEGTYTCRLSPDMPYPLIRTSIKAPGRRLAPEVY 240
Qy 240 MLPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 299
Db 241 MLPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 300
Qy 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 8

US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 91.0%; Score 1691.5; DB 10; Length 342;
Best Local Similarity 90.9%; Pred. No. 8.1e-111;
Matches 311; Conservative 12; Mismatches 18; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSARS 180
Qy 181 RSTK-HHHATTTSITLPPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPCKRLAPEVY 239
Db 181 LVVKEQYNGTFTVSHLPVNTDWDIEGTYTCRLSPDMPYPLIRTSIKAPGRRLAPEVY 240

Qy 240 MLPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 299
Db 241 MLPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 300
Qy 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 9

US-10-176-664-11
; Sequence 11, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match 85.8%; Score 1595; DB 9; Length 341;
Best Local Similarity 85.0%; Pred. No. 4.3e-104;
Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;
Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Db 61 LVDGQAEANLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSASQ 180
Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWRERKKSIGSASQ 180
Qy 181 RSTKHHATTTSITLPPVDAKDWIEGEGYQCRVDHPHPKPIVRSITKLPCKRLAPEVW 240
Db 181 NKDHFNGTITVTSTLPVNTDWDIEGTYTCRVTHPLPKDIVRSIAKLPCKRLAPEVW 240
Qy 241 LPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 300
Db 241 LPPSPETGTTTRVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOKDGTDPSPFL 300
Qy 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 10

US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652

! PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-11

Query Match 85.8%; Score 1595; DB 10; Length 341;
Best Local Similarity 85.0%; Pred. No. 4.3e-104;
Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLSEENITVTVVRERKKSIGSASQ 180
Db 121 KCSESDPRGVTSYLSPPSPDLVYHKAPTICLVVDLATMEGMNLTWYRESKEPVNPGPL 180
Qy 181 RSTKHHTTITSILPVDADKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEYVM 240
Db 181 NKDHFNGTIVTSLPWNVDWIEGEYTCRVTHPLPKDIVRSIAKLPKRLAPEYVM 240
Qy 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSFPLY 300
Db 241 LPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPSFPLY 300
Qy 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 SRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 11
US-10-176-664-10
; Sequence 10, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-10-176-664-10

Query Match 83.7%; Score 1555; DB 9; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120

Db 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RC-SDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLSEENITVTVVRERKKSII--G 176
Db 121 RCTAEESEPRGVSAVLSPTPLDLVYHKSPLKLTCLVLDLASENVNLLWSRKNKGVIILPP 180
Qy 177 SASORSTKHHHTTITSILPVDADKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAP 236
Db 181 PGPPVIKPFQNGTFSATSTLPVNVSDWIEGEYTCNVTHPDLPKPILRSISKLPKRLAP 240
Qy 237 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPS 296
Db 241 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPS 300
Qy 297 FFYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 FFYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 345

RESULT 12
US-09-401-636-10
; Sequence 10, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-10

Query Match 83.7%; Score 1555; DB 10; Length 345;
Best Local Similarity 84.1%; Pred. No. 2.7e-101;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
Qy 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Db 61 LVDQEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIFEDSSR 120
Qy 121 RC-SDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLSEENITVTVVRERKKSII--G 176
Db 121 RCTAEESEPRGVSAVLSPTPLDLVYHKSPLKLTCLVLDLASENVNLLWSRKNKGVIILPP 180
Qy 177 SASORSTKHHHTTITSILPVDADKDWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAP 236
Db 181 PGPPVIKPFQNGTFSATSTLPVNVSDWIEGEYTCNVTHPDLPKPILRSISKLPKRLAP 240
Qy 237 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPS 296
Db 241 EYVMLPPSPETGTRTTCVLRGYPSEISVQWLPNNEEDHTGHTTTRPKQKHGTDPS 300
Qy 297 FFYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 FFYSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 345

RESULT 13
US-10-176-664-8

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; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

Query Match      83.6%; Score 1553.5; DB 9; Length 342;
Best Local Similarity 82.7%; Pred. No. 3.3e-101;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60

Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITOGQWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITOGQWSSNTYTCVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 179
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 179

Qy 180 QRSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 239
Db 180 QRSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 239

Qy 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPFL 299
Db 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPFL 299

Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 15
US-10-176-664-3
; Sequence 3, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

Query Match      82.3%; Score 1529; DB 9; Length 341;
Best Local Similarity 80.6%; Pred. No. 1.7e-99;
Matches 275; Conservative 28; Mismatches 38; Indels 0; Gaps 0;

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Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITOGQWSSNTYTCVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 180
Db 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 180

Qy 181 RSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 240
Db 181 RSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 240

Qy 181 VVKEQYNGTFTVTSHPVNTDDWIEGDTYTCRLSPDMFVPLIRTISKAPGKRLAPEVM 240
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; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

Query Match      83.6%; Score 1553.5; DB 9; Length 342;
Best Local Similarity 82.7%; Pred. No. 3.3e-101;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVW 60
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Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITOGQWSSNTYTCVKHNGSIFEDSSR 120
Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITOGQWSSNTYTCVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDL-ESEENITVTVWRERKKSIGSAS 179
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Qy 180 QRSTKHHAHTTSITSLPVDADKWIEGEGYQCRVDHPPKPIVRSITKLPKRLAPEVY 239
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Qy 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPFL 299
Db 240 MLPSPPEETGTRTTCCLIRGYPSEISVQWLFNNEEDHTGHTTTRPKDGHGTPSPFL 299

Qy 300 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 341
Db 301 YSRMLVNKSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 14
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8
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Db		
301	SRMLVNKSIVEKGNLVTCTRVVHEALPGSRTLEKSLHYSAGN	341
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Db		

Search completed: March 8, 2003, 07:54:18
Job time : 18 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:43:00 ; Search time 38 Seconds
(without alignments)
1195.749 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1858

Sequence: 1 EPHHHHTLSLPESGPVTI.....HEALPGSRTEKLSLHVSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

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4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1840	99.0	341	21	Immunogenic peptid
2	1595	85.8	341	21	Immunogenic peptid
3	1555	83.7	345	21	Immunogenic peptid
4	1539	82.8	342	21	Immunogenic peptid
5	1539	82.8	341	21	Immunogenic peptid
6	1526	82.1	341	21	Opossum IGE heavy
7	1511.5	81.4	342	21	Immunogenic peptid
8	1051	56.6	340	21	Rat IGE heavy chain
9	1012	54.5	313	21	Rat immunoglobulin
10	973	52.4	343	21	Platyus IGE heavy

11	940.5	50.6	421	23	AAU80300	Mouse IGE heavy ch
12	938.5	50.5	426	17	AAU97753	Canine IGE. Canis
13	936	50.4	332	23	AAU80297	Mouse IGE heavy ch
14	936	50.4	332	23	AAU80298	Murine IGE heavy c
15	936	50.4	332	23	AAU80299	Murine IGE heavy c
16	934.5	50.3	417	18	AAU23067	Canine IGE heavy c
17	929.5	50.0	432	23	AAU80294	Murine IGE heavy c
18	925	49.8	343	23	AAU80295	Murine IGE heavy c
19	925	49.8	343	23	AAU80296	Murine IGE heavy c
20	922.5	49.7	312	21	AAV79995	Dog immunoglobulin
21	898	48.3	424	23	AAU50103	Equine IGE heavy c
22	896	48.2	424	23	AAU50104	Equine IGE heavy c
23	862.5	46.4	561	20	AAU17415	Mouse immunoglobul
24	847	45.6	313	21	AAU79997	Mouse immunoglobul
25	745	40.1	323	23	AAU80284	Human IGE heavy ch
26	745	40.1	323	23	AAU80285	Human IGE C2-C3-C4
27	745	40.1	323	23	AAU80286	Human IGE C2-C3-C4
28	745	40.1	324	16	AAU83559	Fc(epsilon) CH2'-C
29	745	40.1	325	16	AAU75225	Human IGE Fc chain
30	745	40.1	325	16	AAU77241	Human IGE Fc chain
31	745	40.1	331	21	AAU803642	Human IGE heavy ch
32	745	40.1	367	9	AAU80291	Interleukin-2/IGE
33	745	40.1	428	23	AAU80283	Human IGE heavy ch
34	745	40.1	428	23	AAU50940	Human IGE epsilon
35	745	40.1	428	23	AAU47863	Human IGE heavy c
36	743	40.0	330	23	AAU80289	Human IGE C2-C3-C4
37	742	39.9	325	21	AAU79994	Human immunoglobul
38	741	39.9	325	16	AAU83582	CH2 to CH4 of huma
39	741	39.9	336	23	AAU80288	Human IGE heavy ch
40	741	39.9	441	23	AAU80287	Human IGE heavy ch
41	737	39.7	493	5	AAU40065	Sequence of human
42	726	39.1	315	16	AAU85582	Fc(epsilon) CH2'-C
43	709	38.2	428	14	AAU42950	Human IGE heavy ch
44	525.5	28.3	245	14	AAU38858	Anti-allergic chim
45	520.5	28.0	468	22	AAU69120	Canine IGE heavy c

ALIGNMENTS

RESULT 1

AAU806206
ID AAB06206 standard; protein; 341 AA.

AAU806206;

22-NOV-2000 (first entry)

Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.

Rat; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;

asthma; eczema; immunogenic peptide.

Chimeric - Didelphis virginiana.

Chimeric - Rattus sp.

WO200025722-A2.

11-MAY-2000.

21-OCT-1999; 99WO-SE01896.

02-NOV-1998; 98US-0106652.

22-SEP-1999; 99US-0401636.

(RESI-) RESISTENTIA PHARM AB.

Hellman LT;

WPI; 2000-365342/31.

Immunogenic polypeptides useful for preventing the harmful effects of

immunoglobulin E in mammals -

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.

SQ Sequence 341 AA;

Query Match 99.0%; Score 1840; DB 21; Length 341;
 Best Local Similarity 99.4%; Pred. No. 1.8e-144;
 Matches 339; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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 Db 1 EPHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHTW 60

Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120
 Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180
 Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Qy 181 RSTKHHTATSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVTM 240
 Db 181 RSTKHHTATSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVTM 240

Qy 241 LPPSPETGTRTTCVCLIRGFYPSISVQWLPNNEEDHTGHHTTRPKDHTGDPSPFLY 300
 Db 241 LPPSPETGTRTTCVCLIRGFYPSISVQWLPNNEEDHTGHHTTRPKDHTGDPSPFLY 300

Qy 301 SRMLVNKSIWEKGNLVCVHVHEALPGSRTLEKSLHYSAGN 341
 Db 301 SRMLVNKSIWEKGNLVCVHVHEALPGSRTLEKSLHYSAGN 341

RESULT 2
 AAB06208
 ID AAB06208 standard; protein; 341 AA.

XX AAB06208;
 XX
 XX
 XX
 XX 22-NOV-2000 (first entry)
 XX
 XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.

XX Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.

XX Chimeric - Didelphis virginiana.
 XX Chimeric - Canis sp.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

XX 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals -

PT

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the dog. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.

SQ Sequence 341 AA;

Query Match 85.8%; Score 1595; DB 21; Length 341;
 Best Local Similarity 85.0%; Pred. No. 3.8e-124;
 Matches 290; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

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Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYCHVKHNGSIFEDSSR 120

Qy 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Db 121 RCDDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVWVRERKKSIGSASQ 180

Qy 181 RSTKHHTATSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVTM 240

Db 181 RSTKHHTATSTSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRKLAPEVTM 240

Qy 241 LPPSPETGTRTTCVCLIRGFYPSISVQWLPNNEEDHTGHHTTRPKDHTGDPSPFLY 300

Db 241 LPPSPETGTRTTCVCLIRGFYPSISVQWLPNNEEDHTGHHTTRPKDHTGDPSPFLY 300

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Db 301 SRMLVNKSIWEKGNLVCVHVHEALPGSRTLEKSLHYSAGN 341

RESULT 3

AAB06207

ID AAB06207 standard; protein; 345 AA.

XX AAB06207;

XX 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.

XX Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.

XX Chimeric - Didelphis virginiana.

XX Chimeric - Sus scrofa.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE01896.

XX 02-NOV-1998; 98US-0106652.

XX 22-SEP-1999; 99US-0401636.

XX (RESI-) RESISTENTIA PHARM AB.

```
PI Hellman LT;
XX WPI; 2000-365342/31.
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals -
XX Disclosure; Fig 2; 50pp; English.
XX The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain
XX constant region 3 from the pig. It was shown to cause a stronger
XX polyclonal anti-self IGE response than peptides consisting of the same
XX regions from one mammal. Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
XX vaccination in humans, against bacterial and viral infections and
XX allergies, such as asthma, fur, pollen and food allergies and eczema.
XX Sequence 345 AA;
Query Match 83.7%; Score 1555; DB 21; Length 345;
Best Local Similarity 84.1%; Pred. No. 8e-121;
Matches 290; Conservative 13; Mismatches 38; Indels 4; Gaps 2;
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Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
Db 61 LVDQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
Qy 121 RC-SDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLSEENITVTVVRERKSI---G 176
Db 121 RCTAEEBPRGSAYLSPTPLDLYHKSPKLTCLVLDLSEENITVTVVRERKSI---G 180
Qy 177 SASQRSTKHHTATSIILPVDADKWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVY 236
Db 181 PGPPVVKPQFGTFSATSLFPVNSDWEGETTYCNVTHPDLPKPILRSISKLPKRLAP 240
Qy 237 EVMYLPSPSEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPS 296
Db 241 EVMYLPSPSEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPS 300
Qy 297 FFLYSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 341
Db 301 FFLYSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 345
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AAB06205
ID AAB06205 standard; protein; 342 AA.
XX AC AAB06205;
XX AC AAB06205;
XX DT 22-NOV-2000 (first entry)
XX DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
XX KW Human; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
XX KW asthma; eczema; immunogenic peptide.
XX OS Chimeric - Didelphis virginiana.
XX OS Chimeric - Homo sapiens.
XX PN WO200025722-A2.
XX XX
XX FD 11-MAY-2000.
XX XX
XX PF 21-OCT-1999; 99WO-SE01896.
XX PR 02-NOV-1998; 98US-0106652.
XX PR 22-SEP-1999; 99US-0401636.
XX XX
XX PA (RESI-) RESISTENTIA PHARM AB.
XX PI Hellman LT;
XX DR WPI; 2000-365342/31.
XX PT Immunogenic polypeptides useful for preventing the harmful effects of
XX PT immunoglobulin E in mammals -
XX PS Disclosure; Fig 2; 50pp; English.
XX PS The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2 and 4 of the opossum IGE and the heavy chain
XX constant region 3 from the human. It was shown to cause a stronger
XX polyclonal anti-self IGE response than peptides consisting of the same
XX regions from one mammal. Immunogenic peptides, particularly those
XX consisting of different heavy chain constant regions, can be used for
XX vaccination in humans, against bacterial and viral infections and
XX allergies, such as asthma, fur, pollen and food allergies and eczema.
XX SQ Sequence 342 AA;
Query Match 83.6%; Score 1553.5; DB 21; Length 342;
Best Local Similarity 82.7%; Pred. No. 1.1e-120;
Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;
Qy 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Db 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVW 60
Qy 61 LVDQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
Db 61 LVDQEAENLPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
Qy 121 RCSDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLSEENITVTVVRERKSI--GAS 179
Db 121 KCADSNPRGSAYLSRSPFDLFIKSPITITCLVVDLAPSGTGNLTWSRSGKPVNHS 180
Qy 180 QRSTKHHTATSIILPVDADKWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVY 239
Db 181 RKEKQRNGTITVTSTPLPVGTRDMEGETYQCRVTHPLPALMRSTTKLPKRLAPEVY 240
Qy 240 MLPSPSEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFL 299
Db 241 MLPSPSEETGTRTTCCLIRGYPSEISVQWLPNNEEDHTGHTTTRPQKHGTDPSFFL 300
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Db 301 YSRMLVNKSIWEKGNLTCRVVHEALPGSRTLKSLHYSAGN 342
RESULT 5
AAB06202
ID AAB06202 standard; protein; 341 AA.
XX AC AAB06202;
XX AC AAB06202;
XX DT 22-NOV-2000 (first entry)
XX DE Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.
XX KW Mouse; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
XX KW asthma; eczema; immunogenic peptide.
XX OS Chimeric - Didelphis virginiana.
XX OS Chimeric - Mus sp.
XX PH Key Location/Qualifiers
XX FT Misc-difference 1..341
XX FT /label= OTHER
XX FT /note= "Xaa=unknown"
XX FT
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PN WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SE01896.
 XX 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 PA Hellman LT;
 XX WPI; 2000-365342/31.
 DR Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX Disclosure; Fig 2; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the mouse. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX Sequence 341 AA;

Query Match 82.8%; Score 1539; DB 21; Length 341;
 Best Local Similarity 85.9%; Pred. No. 1.7e-119;
 Matches 293; Conservative 12; Mismatches 34; Indels 2; Gaps 2;
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 Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
 Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
 Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
 Qy 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 Db 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 179
 Qy 181 RSTKHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
 Db 180 WYTKHHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 239
 Qy 240 MLPPSPDEGTTRTVTCLIRGYPSEISVQWLPNNDEHTGHHTTRPKDGTDPSPFL 299
 Db 240 MLPPSPDEGTTRTVTCLIRGYPSEISVQWLPNNDEHTGHHTTRPKDGTDPSPFL 299
 Qy 300 YSRMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340
 Db 300 YSRMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340

RESULT 6
 AAB03644
 ID AAB03644 standard; protein; 341 AA.
 AC AAB03644;
 XX 22-NOV-2000 (first entry)

DE Opossum IgE heavy chain constant regions 2, 3 and 4.
 XX Opossum; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.

OS Didelphis virginiana.
 XX WO200025722-A2.
 XX 11-MAY-2000.
 XX 21-OCT-1999; 99WO-SE01896.
 XX 02-NOV-1998; 98US-0106652.
 PR 22-SEP-1999; 99US-0401636.
 XX (RESI-) RESISTENTIA PHARM AB.
 PA Hellman LT;
 XX WPI; 2000-365342/31.
 DR Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX Disclosure; Fig 1; 50pp; English.
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2, 3 and 4 of the opossum IgE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IgE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IgE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.
 XX Sequence 341 AA;

Query Match 82.1%; Score 1526; DB 21; Length 341;
 Best Local Similarity 80.4%; Pred. No. 2e-118;
 Matches 274; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
 Qy 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
 Db 1 EFHHHHHTLSLPESGPVTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTV 60
 Qy 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
 Db 61 LVDGQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTVCHVKNHGSIFEDSSR 120
 Qy 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 Db 121 RCDDEPRGVITLPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQ 180
 Qy 181 RSTKHHAHTTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPKRLAPEVY 240
 Db 181 VVKEQYNGTFTVTSHLPVNTDDWIEGDTYTCRLESPPDVPVPLIRTISKAPGKRLAPEVY 240
 Qy 241 LPPSPDEGTTRTVTCLIRGYPSEISVQWLPNNDEHTGHHTTRPKDGTDPSPFL 300
 Db 241 LPPSPDEGTTRTVTCLIRGYPSEISVQWLPNNDEHTGHHTTRPKDGTDPSPFL 300
 Qy 301 SRMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 341
 Db 301 SRMLVKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 341

RESULT 7
 AAB06201
 ID AAB06201 standard; protein; 342 AA.
 AC AAB06201;
 XX 22-NOV-2000 (first entry)

DE Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.
 KW asthma; eczema; immunogenic peptide.

KW Rat; opoosum; immunoglobulin E; IgE; vaccination; infection; allergy;
 XX asthma; eczema; immunogenic peptide.
 OS Chimeric - Didelphis virginiana.
 OS Chimeric - Rattus sp.
 XX Key Location/Qualifiers
 PH Misc-difference 1..342
 FT /label= OTHER
 FT /note= "Xaa=unknown"
 PT
 XX WO200025722-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 21-OCT-1999; 99WO-SE01896.
 XX
 XX 02-NOV-1998; 98US-0106652.
 PR
 XX 22-SEP-1999; 99US-0401636.
 XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA
 XX Hellman LT;
 XX
 XX WPI; 2000-365342/31.
 XX
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX
 XX Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 created from a combination of the one from the rat
 CC and the one from the opossum. It was shown to cause a stronger
 CC polyclonal anti-self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 XX
 SQ Sequence 342 AA;
 Query Match 81.4%; Score 1511.5; DB 21; Length 342;
 Best Local Similarity 83.6%; Pred. No. 3.2e-117;
 Matches 285; Conservative 16; Mismatches 39; Indels 1; Gaps 1;
 QY 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTW 60
 DB 1 EFHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTW 60
 QY 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQQWMSNTYTVCHVKNHGSIPEDSSR 120
 DB 61 LVDGQAEALFPYTRPKREGGQTFSLQSEVNITQQWMSNTYTVCHVKNHGSIPEDSSR 120
 QY 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGTSASQ 180
 DB 121 RCDDEPRGVITYLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGTSASQ 180
 QY 181 RSTKH-HHATTSITSLIPVDADKMEGEGYQCRVDHPFPKPIVRSITKLPKRLAPVY 239
 DB 181 LVVKEHYHGTFTXSHLPVEDDDMEGTYTXLLESPPMIVILPTISALPGKRLAPVY 240
 QY 240 MLPPSPETGTRTITVTLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 299
 DB 241 MLPPSPETGTRTITVTLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFL 300
 QY 300 YSRMLVNHKSWEKGNLVTCTVWVHEALPGSRTLKSLHYSAG 340
 DB 301 YSRMLVNHKSWEKGNLVTCTVWVHEALPGSRTLKSLHYSAG 341

RESULT 8

AAB03643
 ID AAB03643 standard; protein; 340 AA.
 XX
 AC AAB03643;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Rat IgE heavy chain constant regions 2, 3 and 4.
 XX
 KW Rat; immunoglobulin E; IgE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX
 OS Rattus sp.
 XX
 XX WO200025722-A2.
 XX
 XX 11-MAY-2000.
 XX
 XX 21-OCT-1999; 99WO-SE01896.
 XX
 XX 02-NOV-1998; 98US-0106652.
 PR
 XX 22-SEP-1999; 99US-0401636.
 XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA
 XX Hellman LT;
 XX
 XX WPI; 2000-365342/31.
 XX
 XX Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX
 XX Disclosure; Fig 1; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2, 3 and 4 of the rat IgE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC anti-self IgE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.
 XX
 SQ Sequence 340 AA;
 Query Match 56.6%; Score 1051; DB 21; Length 340;
 Best Local Similarity 62.6%; Pred. No. 5.2e-79;
 Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;
 QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTTWLDGQAEALFPYTR 76
 DB 8 PVNITKPTVDLLHSSCDPNA-FHSTIQLCYFVYGHQNDVSIHMLMDRKi-----YETH 61
 QY 77 PK----REGGQTFSLQSEVNITQQWMSNTYTVCHVKNHGSIPEDSSRCDDEPRGVIT 132
 DB 62 AQNVLIKEEGKLASTYSLRNITQQWMSSEFTCKVTSQGENYWAHTRCRSDDEPRGVIT 121
 QY 133 YLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGTSASORSTKHHHATTSI 192
 DB 122 YLIPSPDLVYENGTPKLTCLVLDLESEENITVTVWRERKKSIGTSASORSTKHHHATTSI 181
 QY 193 TSILPVDADKMEGEGYQCRVDHPFPKPIVRSITKLPKRLAPVYMLPPSPETGTR 252
 DB 182 TSILPVDADKMEGEGYQCRVDHPFPKPIVRSITKLPKRLAPVYMLPPSPETGTR 241
 QY 253 TVTCLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVNHKSWEK 312
 DB 242 TLTCLIQNFPEIDISVQWLPQSLPKPSQHSHTTTPKYNQSGNORFFIFSRLEVTKALWTQ 301
 QY 313 GNLVTCRVVHEALPGSRTLKSLHYSAGN 341
 DB 302 TKQFTCRVHEALREPRKLERKTSKSLGN 330

RESULT 9	
AAAY79996	
ID	AAAY79996 standard; Protein; 313 AA.
XX	
AC	AAAY79996;
XX	
XX	15-MAY-2000 (first entry)
XX	
DE	Rat immunoglobulin E epsilon heavy chain SEQ ID NO:3.
DE	
XX	Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW	immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW	antibody; allergy; allergic disease; immunisation; anti-allergic;
KW	anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX	
OS	Rattus sp.
XX	
PN	WO9967293-A1.
XX	
PD	29-DEC-1999.
XX	
PF	21-JUN-1999; 99WO-US13959.
XX	
PR	20-JUN-1998; 98US-0100287.
XX	
PA	(UNBI-) UNITED BIOMEDICAL INC.
XX	
PI	Wang CY, Walfield AM;
XX	
XX	WPI; 2000-160578/14.
DR	
PT	New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT	for immunization against allergy -
XX	
PS	Example 1; Page 66-68; 155pp; English.
XX	
CC	The present invention describes immunoglobulin E (IgE)-CH3 domain
CC	antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic
CC	and anti-asthmatic properties. (I) induces polyclonal antibodies
CC	specific for a target effector site on the epsilon-heavy chain of IgE,
CC	and so preventing triggering and activation of mast cells and basophils
CC	and downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC	containing (I) are used for active immunisation against IgE-mediated
CC	allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC	dermatitis. Nucleic acids that encode these compounds are useful for
CC	recombinant production of corresponding peptides or in DNA vaccines.
CC	Conjugates of (I) that include a promiscuous T helper cell epitope
CC	(functional in genetically diverse subjects), in addition to a B cell
CC	target epitope, have increased immunogenicity and may include cyclic
CC	constraints (disulfide bridge) to stabilise conformational features and
CC	maximize cross-reactivity to the natural target. They induce safe
CC	(non-anaphylactogenic) antibodies. AAAY79994 to AAAY80084 represent amino
CC	acid sequences used in the exemplification of the present invention.
XX	
XX	Sequence 313 AA;
XX	
Query Match	54.5%; Score 1012; DB 21; Length 313;
Best Local Similarity	63.3%; Pred. No. 8e-76;
Matches	198; Conservative
QY	17 PVTIIPTVKLFHSCDPRGDAHSTIQLLLCVLSGFSPAKVHVTVLVLDQGEAENLFPYVTR 76
Db	3 PVNITKPTVDLLHSSCDPNA-FHSTIQLYCFYGHQIDVSIHMLMDRDKI-----YDTH 56
QY	77 PK----REGGTFSLQSRVNTICQWMSNTYTCVHKNGSIFEDSSRRCSDDEPRGVIT 132
Db	57 AQNVLIKEEGKLASTYKRLNITCQWMSSETFTCKVTSQGNVWHTSRRCSDDEPRGVIT 116
QY	133 YLIPPSLDLYENGTPKLTCLVLVLESEENTVTVWRERKKSIGSASORSTKHHATTSI 192
Db	117 YLIPPSLDLYENGTPKLTCLVLVLESEENTVTVWRERKKSIGSASORSTKHHATTSI 176

CC vital systems. The IgE can be used in drug development (e.g.
 CC small molecule screening, assay development and anti-IgE
 CC antibody generation). Fragments of IgE can be used in vaccines
 CC or to prevent IgE-mediated hypersensitivity. The new sequence
 CC information permits targeted modulation of IgE-mediated immune
 CC responses.

XX Sequence 426 AA;

Qy 18 VTIIPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGQAEANLPYTTTP 77
 Db 102 LNFIPPTVKLFHSSCNPGVDHTTIIQLCLISGYVPGDMEVILVDGQKATNIPYTAGP 161
 Qy 78 KREGGOTFSQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRRCSDDPRGVITLIPP 137
 Db 162 TKEGNT-STHSEINITQGEWSQKTYTCQVYQGFTEKDEARKSESDPRGVSTLSP 220
 Qy 138 SPLDYENGTPKLTCLVLDLESEENITVWVRERKKSIGASQSRSTKHHTTSITSLP 197
 Db 221 SPLDYVHKAPKITCLVLDLATMEGNLTWYRESKEPVNPGPLNKKDHPNGITVTSTLP 280
 Qy 198 VDADKWIIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPEVYMLPPSPBETGTR--TVT 255
 Db 281 VNTNDWIEGETYTCRVTHPLPKDIVRSIAKAPGRAPDVPVYLFPPERQOQTKDORVTLT 340
 Qy 256 CLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVKNKSIWEKGNL 315
 Db 341 CLIQNFADISVQWLNDSPDTQDTYTTGPHKVGSRPAFFISRLVSRVDNEQKNK 400
 Qy 316 VTCRVVHEALPGSRITLKSLSHYSAG 340
 Db 401 FTCQVHEALSGSRILQKWSKTPG 425

RESULT 13

AAU80297

ID AAU80297 standard; Protein; 332 AA.

XX AC

XX AC

XX DT 30-JUL-2002 (first entry)

XX DE

XX DE Mouse IgE heavy chain C2-C3-C4 domain with MIGIS fragment.

XX KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain; MIGIS.

XX OS

XX OS

XX OS Synthetic.

XX FN WO200220038-A2.

XX PD 14-MAR-2002.

XX PF 06-SEP-2001; 2001WO-DK00579.

XX XX 06-SEP-2000; 2000DK-0001326.

PR 15-SEP-2000; 2000US-232831P.

XX XX (PHAR-) PHARMEXA AS.

XX PI Klysner S, Von Hoegen P, Voldborg B, Gautam A;

XX WPI; 2002-383033/41.

XX DR, Inducing immune response against autologous immunoglobulin E in an

PT animal, by effecting simultaneous presentation of cytotoxic T

PT lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
 PT Examples; Page 137-138; 151pp; English.

CC This invention relates to a novel method for inducing an immune response
 CC against autologous immunoglobulin E (IgE) in an animal. The method
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell
 CC epitope (TH epitope) which is foreign to the animal, by antigen
 CC presenting cells (APCs) of the animal's immune system. The epitopes
 CC of the invention may be used as a vaccine against allergic diseases. The
 CC method of the invention is useful for inducing an immune response
 CC against autologous IgE in an animal, which is useful for downregulating
 CC autologous IgE in the animal. This method is useful in the prevention
 CC and treatment of allergic diseases such as anaphylaxis, allergic
 CC rhinitis, asthma and atopic dermatitis. The present sequence represents
 CC the mouse IgE heavy chain C2-C3-C4 domain with the MIGIS fragment used
 CC to create the epitopes used in the method of the invention.

XX Sequence 332 AA;

Qy Query Match 50.4%; Score 936; DB 23; Length 332;

Best Local Similarity 56.7%; Pred. No. 1.8e-69;

Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;

Qy 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLVDGQAEANLPYTTTP 76

Db 4 PVNITEPTLELLHSSCDPNA-FHSTIQLYCFYGHILNDVSVSLMDREITDTLTAQTVL 62

Qy 77 PKREGGOTFSQSEVNITQGMSSNTYTCHVKHNGSIFEDSSRRCSDDPRGVITLIPP 136

Db 63 IKEE-GKLAUASCUNITEQMMSESTFKVTSGVYLAHTRCPDHPHGVITLIPP 121

Qy 137 PSLDYENGTPKLTCLVLDLESEENITVWVRERKKSIGASQSRSTKH-HATTSITSI 195

Db 122 PSLDLYQNGAPKLTCLVLDLESEKNVNTWQEKTSV-SASQWYTKHNNATTSITSI 180

Qy 196 LPVDADKWIIEGEGYQCRVDHHPFKPIVRSITKLPKGLAPEVYMLPPSPBETGTRTVT 255

Db 181 LPVVAKDWIIEGYQCVVDHDPFKPIVRSITKTPQRSAPVYVFPPEESEDKRTLT 240

Qy 256 CLIRGFYSEISVQWLPNNEEDHTGHTTTRPKDGHGTDPSFFLYSRMLVKNKSIWEKGNL 315

Db 241 CLIQNFADISVQWLNDSPDTQDTYTTGPHKVGSRPAFFISRLVSRVAKTLWTQRKQ 300

Qy 316 VTCRVVHEALPGSRITLKSLSHYSAGN 341

Db 301 FTCQVHEALQKPKLEKTISTSLGN 326

RESULT 14

AAU80298

ID AAU80298 standard; Protein; 332 AA.

XX AC

XX AC

XX DT 30-JUL-2002 (first entry)

XX DE

XX DE Murine IgE heavy chain C2-C3-C4 for mammalian expression.

XX KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
 KW heavy chain C domain.

XX OS

XX OS Synthetic.

XX FN WO200220038-A2.

XX PD 14-MAR-2002.

06-SEP-2001; 2001WO-DK00579.
06-SEP-2000; 2000DK-0001326.
15-SEP-2000; 2000US-232831P.
(PHAR-) PHARMEXA AS.
Klyener S, Von Hoegen P, Voldborg B, Gautam A;
WPI; 2002-383033/41.
N-PSDB; ABK51141.
Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
Disclosure; Page 140-141; 151pp; English.
This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the mouse IgE heavy chain C2-C3-C4 domain optimised for a mammalian expression system used to create the epitopes used in the method of the invention.
Sequence 332 AA;
Query Match 50.4%; Score 936; DB 23; Length 332;
Best Local Similarity 56.7%; Pred. No. 1.8e-69;
Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;
QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLWDQGEAENLPFYTR 76
Db 4 PWNITEPTLELLHSSCDPNA-FHSTIQLCYFYGHILNDVSVSLMDREITDTLAQTVL 62
QY 77 PKREGGQTFSLQSEVNITQGWMSNTVTCVKHNGSIFEDSSRRCSDEPRGVITYLIP 136
Db 63 IKEE-GKLASTCSKLNITEQWMSSTFTCKVTSQGVLDYLAHTRCPDHEPRGVITYLIP 121
QY 137 PSLDLYENGTPKLTCLVLDLESENIITVWRERKKSIGSASQSRSTKH-HATTSTISI 195
Db 122 PSLDLYQNGAPKLTCLVLDLESEKNVNTWNEKTSV-SASQWYTKHNNATTSITI 180
QY 196 LPVDAKWIEGEGYQCRVDHPFKPIVRSITKLPGRKLAPEVYMLPSPETGTRTVT 255
Db 181 LPVAKWIEGYGQICVDHPDFPKPIVRSITKTPGQSAPEVYVFPPESEDKRTL 240
QY 256 CLIRGFYPSISVQWLPNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNKSIWEKGNL 315
Db 241 CLIQNFPPEDISVQWLGDKLINSQHSITTPKSGNSQGFIFSRLEVAKLWTQRQ 300
QY 316 VTCRVVHEALPGSRFTLEKSLHYSAGN 341
Db 301 FTCQVTHEALQPKRLEKTIISTISLGN 326
RESULT 15
AAU80299
ID AAU80299 standard; Protein; 332 AA.
XX
AC AAU80299;
XX
DT 30-JUL-2002 (first entry)

XX Murine IgE heavy chain C2-C3-C4 for E.Coli expression.
DE
XX
KW IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic;
KW antiaesthetic; dermatological; antiinflammatory; immunoglobulin E; IgE;
KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
KW heavy chain C domain.
XX
OS Mus sp.
OS Synthetic.
XX
PN W0200220038-A2.
XX
PD 14-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-DK00579.
XX
PR 06-SEP-2000; 2000DK-0001326.
PR 15-SEP-2000; 2000US-232831P.
XX
PA (PHAR-) PHARMEXA AS.
XX
PI Klyener S, Von Hoegen P, Voldborg B, Gautam A;
XX
XX WPI; 2002-383033/41.
DR N-PSDB; ABK51142.
XX
Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin
Disclosure; Page 144-145; 151pp; English.
This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the mouse IgE heavy chain C2-C3-C4 domain optimised for an E.Coli expression system used to create the epitopes used in the method of the invention.
Sequence 332 AA;
Query Match 50.4%; Score 936; DB 23; Length 332;
Best Local Similarity 56.7%; Pred. No. 1.8e-69;
Matches 185; Conservative 46; Mismatches 91; Indels 4; Gaps 4;
QY 17 PVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHVTVLWDQGEAENLPFYTR 76
Db 4 PWNITEPTLELLHSSCDPNA-FHSTIQLCYFYGHILNDVSVSLMDREITDTLAQTVL 62
QY 77 PKREGGQTFSLQSEVNITQGWMSNTVTCVKHNGSIFEDSSRRCSDEPRGVITYLIP 136
Db 63 IKEE-GKLASTCSKLNITEQWMSSTFTCKVTSQGVLDYLAHTRCPDHEPRGVITYLIP 121
QY 137 PSLDLYENGTPKLTCLVLDLESENIITVWRERKKSIGSASQSRSTKH-HATTSTISI 195
Db 122 PSLDLYQNGAPKLTCLVLDLESEKNVNTWNEKTSV-SASQWYTKHNNATTSITI 180
QY 196 LPVDAKWIEGEGYQCRVDHPFKPIVRSITKLPGRKLAPEVYMLPSPETGTRTVT 255
Db 181 LPVAKWIEGYGQICVDHPDFPKPIVRSITKTPGQSAPEVYVFPPESEDKRTL 240
QY 256 CLIRGFYPSISVQWLPNNEEDHTGHTTTRPKQDHGTDPSFFLYSRMLVNKSIWEKGNL 315

Db 241 CLIQFFPDISVQWLGDKLISNSQHSSTTTPKSGNSQGFIFSRLEVAKTLWTQRKQ 300

Qy 316 VTCRVVHEALPGSRTLEKSLHYSAGN 341

Db 301 FTCQVIHEALQKPRKLEKTISTSLGN 326

Search completed: March 8, 2003, 07:48:13
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:46:20 ; Search time 33 Seconds
(without alignments)
2129.154 Million cell updates/sec

Title: US-09-401-636-4
Perfect score: 1958
Sequence: 1 EFRHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHYSAGN 341

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 21:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phage:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	488.5	26.3	375	4 Q9BSZ1	Q9bsz1 homo sapien
2	488.5	26.3	588	4 Q8WUX4	Q8wux4 homo sapien
3	488.5	26.3	597	4 Q9BQ88	Q9bqb8 homo sapien
4	488.5	26.3	597	4 Q96BB9	Q96bb9 homo sapien
5	488.5	26.3	597	4 Q9BU10	Q9bul10 homo sapien
6	488.5	26.3	613	4 Q96EY0	Q96ey0 homo sapien
7	488.5	26.3	613	4 Q8WUK1	Q8wuk1 homo sapien
8	488.5	26.3	614	4 Q96GAK	Q96ga6 homo sapien
9	488.5	26.3	618	4 Q96AA6	Q96aa6 homo sapien
10	463	24.9	337	6 Q95M34	Q95m34 equus caball
11	455.5	24.5	613	11 Q8VCX7	Q8vcx7 mus musculus
12	455	24.5	473	4 Q8TC63	Q8tc63 homo sapien
13	441.5	23.8	471	4 Q8TC77	Q8tc77 homo sapien
14	435	23.4	437	11 Q9RIA4	Q9ria4 mus musculus
15	434.5	23.4	463	11 Q99IC4	Q99ic4 mus musculus
16	429.5	23.1	469	11 Q8R3V9	Q8r3v9 mus musculus

17	424.5	22.8	473	11 Q9DBL4	Q9dbl4 mus musculus
18	406	21.9	473	11 Q91Z05	Q91z05 mus musculus
19	406	21.9	474	11 Q8R3H6	Q8r3h6 mus musculus
20	400.5	21.6	468	11 Q99L31	Q99l31 mus musculus
21	400.5	21.6	473	11 Q99L25	Q99l25 mus musculus
22	390	21.0	701	4 Q96RQ8	Q96pq8 homo sapien
23	355	19.1	416	4 Q9NPP6	Q9npp6 homo sapien
24	347.5	18.7	384	4 Q9UP60	Q9up60 homo sapien
25	346.5	18.6	494	4 Q96K68	Q96k68 homo sapien
26	346.5	18.6	496	4 Q96KX8	Q96kx8 homo sapien
27	345.5	18.6	496	4 Q96DK0	Q96dk0 homo sapien
28	344.5	18.5	497	4 Q8WY24	Q8wy24 homo sapien
29	336.5	18.1	500	4 Q9BRV0	Q9brv0 homo sapien
30	333.5	17.9	426	11 Q9DCD9	Q9dcd9 mus musculus
31	330.5	17.8	486	11 Q91Z07	Q91z07 mus musculus
32	330.5	17.8	487	11 Q99KA4	Q99ka4 mus musculus
33	326	17.5	479	11 Q99M22	Q99m22 mus musculus
34	326	17.5	481	11 Q8VCV5	Q8vcv5 mus musculus
35	326	17.5	484	11 Q99LA6	Q99la6 mus musculus
36	322.5	17.4	684	13 Q90544	Q90544 ginglymoato
37	314	16.9	488	11 Q91WR1	Q91wr1 mus musculus
38	314	16.9	489	11 Q8VCX4	Q8vcx4 mus musculus
39	313	16.8	481	11 Q91WT3	Q91wt3 mus musculus
40	313	16.8	481	11 Q91WT1	Q91wt1 mus musculus
41	313	16.8	482	11 Q91X92	Q91x92 mus musculus
42	313	16.8	484	11 Q8VEA0	Q8ves0 mus musculus
43	312	16.8	480	11 Q91XE1	Q91xe1 mus musculus
44	311	16.7	479	11 Q91WP5	Q91wp5 mus musculus
45	210	11.3	573	4 Q8WU38	Q8wu38 homo sapien

ALIGNMENTS

RESULT 1

Q9BSZ1	ID	Q9BSZ1	PRELIMINARY;	PRT;	375 AA.
AC	Q9BSZ1;				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)			
DE	Hypothetical 41.3 KDa protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lymph;				
RA	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
RL	EMBL; BC004476; AAH04476.1; -				
DR	HSP; P01857; IFC1.				
DR	InterPro; IPR003597; Ig_c1.				
DR	InterPro; IPR003600; Ig_like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; Ig; 3.				
DR	SMART; SM00407; IGc1; 3.				
DR	SMART; SM00410; IG_like; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.				
KW	Hypothetical protein.				
SQ	SEQUENCE 375 AA; 41314 MW; B1A0A0998F473619 CRC64;				

Query Match 26.3%; Score 488.5; DB 4; Length 375;

Best Local Similarity 31.2%; Pred.No. 2.2e-37; Mismatches 134; Indels 25; Gaps 10;

Matches 105; Conservative 73;

Qy 17 PVTII---PPVTKLFFHSSCDPR----GDAHSTIQLLCVSGFSAPKAVHTVLVDQAEAN 69

Db 24 PLPIAELPPKVSF---VPRDGFEGNPKS-KLICATGFSRQIQVSMLEKQVGS 79

Qy 70 LFPVTT-----RPKREGQTFSLQSEVNTITQGMSSNTYTCVHKNGSIF-EQSSRRCS 123

Db 80 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 137
Qy 124 DDEPRGVITYLPPSPDLIYENGTKLCLVLDSSEENITVTVRERKKSIGSASQST 183
Db 138 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTYDSVTSWTRQNGEAVKHTNISE 197
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 198 SHPNATFSAVGEASICEDDWSGERFTCTVTHDLPSPKQTIISRPKGVALLHRPVDYLLP 257
Qy 243 PPSPEETG--TTRTVTLIRGFFYPSISVQWLPNNBEDHTGHHTTTRPKQKHGTDPSPFLY 300
Db 258 PAREQLNRESATITCLVTGFSADVFVQWQMGQPLSPEKYVTSAPMEPQAPGRYFAH 317
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 318 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 354

RESULT 2

Q8WUX4 PRELIMINARY; PRT; 588 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 64.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=LYMPH;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG.5.
DR SMART; SM00409; IG.2.
DR SMART; SM00407; IGcl.4.
DR SMART; SM00406; IGv.1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;

Query Match 26.3%; Score 488.5; DB 4; Length 588;
Best Local Similarity 31.2%; Pred.No. 4.1e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;
Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTLVDQGEAEN 69
Db 246 PLPVIAELPPKVSVP---VPPRDGFFGNPKS-KLICQATGFSRQIQVSWLREGKQVGS 301
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHGSIP-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 359
Qy 124 DDEPRGVITYLPPSPDLIYENGTKLCLVLDSSEENITVTVRERKKSIGSASQST 183
Db 360 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTYDSVTSWTRQNGEAVKHTNISE 419
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 420 SHPNATFSAVGEASICEDDWSGERFTCTVTHDLPSPKQTIISRPKGVALLHRPVDYLLP 479
Qy 243 PPSPEETG--TTRTVTLIRGFFYPSISVQWLPNNBEDHTGHHTTTRPKQKHGTDPSPFLY 300
Db 480 PAREQLNRESATITCLVTGFSADVFVQWQMGQPLSPEKYVTSAPMEPQAPGRYFAH 539

Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 576
RESULT 3
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (protein for MGC:1905) (protein for MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=MUSCLE;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR EMBL; BC001872; AAH01872.1; -
DR HSSP; P01825; 7PAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003600; IG.like.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG.5.
DR SMART; SM00409; IG.2.
DR SMART; SM00407; IGcl.4.
DR SMART; SM00406; IGv.1.
DR SMART; SM00410; IG.like.1.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 26.3%; Score 488.5; DB 4; Length 597;
Best Local Similarity 31.2%; Pred.No. 4.2e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTLVDQGEAEN 69
Db 246 PLPVIAELPPKVSVP---VPPRDGFFGNPKS-KLICQATGFSRQIQVSWLREGKQVGS 301
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGMSSNTYTCHVKHGSIP-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTITIKESDWLSQSMTFCRVDRHGLTFOQNASSMCV 359
Qy 124 DDEPRGVITYLPPSPDLIYENGTKLCLVLDSSEENITVTVRERKKSIGSASQST 183
Db 360 PQDQTAIRFAIPSPFASIFLTKSLKTLCLVTLDTLTYDSVTSWTRQNGEAVKHTNISE 419
Qy 184 KHHATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRISITKLPKRL-APEVYMLP 242
Db 420 SHPNATFSAVGEASICEDDWSGERFTCTVTHDLPSPKQTIISRPKGVALLHRPVDYLLP 479
Qy 243 PPSPEETG--TTRTVTLIRGFFYPSISVQWLPNNBEDHTGHHTTTRPKQKHGTDPSPFLY 300
Db 480 PAREQLNRESATITCLVTGFSADVFVQWQMGQPLSPEKYVTSAPMEPQAPGRYFAH 539
Qy 301 SRMLVNSIWEKGNLVTCTRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 576

RESULT 4


```
Q96BB9          PRELIMINARY;      PRT;    597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 65.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CCELL;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8BCE263D9 CRC64;

Query Match      26.3%; Score 488.5; DB 4; Length 597;
Best Local Similarity 31.2%; Pred. No. 4.2e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAEN 69
Db 246 PLPVAIELPPKVSVP---VPRDGFNGPRKS-KLICATGFSFQIQVSWLREGKQVGS 301
Qy 70 LFPYTT-----RPKREGQTFSLOSEVNIQTQGMSSNTYTCVHKNGSIF-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTIKESDMLSQSMFTCRVDHRLGLTFQONASSMCV 359
Qy 124 DDEPRGVITYLIPSPDLNYGTPKLTCLVLDSEENITVWVRKKSIGSASQST 183
Db 360 PQDQTAIRVAIPSPFASIFLTKSTKLTCLVTLDTLTYDSVTISWTRQNGEAVKTHNISE 419
Qy 184 KHHATTISITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPCKRL-APEVYMLP 242
Db 420 SHPNATFSVAGEASICEDDMSNGERFTCTVTHDLPSPKQITSRPKGVALHRPDPVLLP 479
Qy 243 PSPBETG--TTRVTCLIRGYPSPISVQWLPNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 480 PAREQLNLRRESATITCLVTGSPADVFQWMQGOPLSPEKYVTSAPMPEQAPGRYFAH 539
Qy 301 SRMLVNSIWEKGNLVTCRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEMWTGTYTCVAHEALPNRVTRTVDKS 576

RESULT 5
Q9BU10          PRELIMINARY;      PRT;    597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 65.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSP; P01825; 7FAB
DR InterPro; IPR003597; IG_c1.
DR
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DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match      26.3%; Score 488.5; DB 4; Length 597;
Best Local Similarity 31.2%; Pred. No. 4.2e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAEN 69
Db 246 PLPVAIELPPKVSVP---VPRDGFNGPRKS-KLICATGFSFQIQVSWLREGKQVGS 301
Qy 70 LFPYTT-----RPKREGQTFSLOSEVNIQTQGMSSNTYTCVHKNGSIF-EDSSRRCS 123
Db 302 --GVTTDQVQAEAKESGPTTYKVTSTLTIKESDMLSQSMFTCRVDHRLGLTFQONASSMCV 359
Qy 124 DDEPRGVITYLIPSPDLNYGTPKLTCLVLDSEENITVWVRKKSIGSASQST 183
Db 360 PQDQTAIRVAIPSPFASIFLTKSTKLTCLVTLDTLTYDSVTISWTRQNGEAVKTHNISE 419
Qy 184 KHHATTISITSLPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPCKRL-APEVYMLP 242
Db 420 SHPNATFSVAGEASICEDDMSNGERFTCTVTHDLPSPKQITSRPKGVALHRPDPVLLP 479
Qy 243 PSPBETG--TTRVTCLIRGYPSPISVQWLPNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 480 PAREQLNLRRESATITCLVTGSPADVFQWMQGOPLSPEKYVTSAPMPEQAPGRYFAH 539
Qy 301 SRMLVNSIWEKGNLVTCRVVHEALPG---SRTLEKS 334
Db 540 SILTVSEEMWTGTYTCVAHEALPNRVTRTVDKS 576

RESULT 6
Q96EYO          PRELIMINARY;      PRT;    613 AA.
AC Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:20337).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CCELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.1; -.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match      26.3%; Score 488.5; DB 4; Length 613;
Best Local Similarity 31.2%; Pred. No. 4.3e-37;
Matches 105; Conservative 73; Mismatches 134; Indels 25; Gaps 10;

Qy 17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPAKVHVTVLVDQGEAEN 69
Db 246 PLPVAIELPPKVSVP---VPRDGFNGPRKS-KLICATGFSFQIQVSWLREGKQVGS 301
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Db 241 PLPVIAELPPKVSVF---VPPRDGFFGNPKRS-KLICQATGFSPPQIQVSWLREGQVGS 296
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRRCS 123
Db 297 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 354
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 355 PQDQTAIRVFAIPSPFASIFLTSTLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 414
Qy 184 KHHATTTSITSLPVDADKWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 415 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALHRPVDYLLP 474
Qy 243 PSPETG---TTRTVTCLIRGFPSEISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 475 PAREQLNRESATITCLVTGFSFADVFQWMQRGOPLSPEKYVTSAPMPPEQAPGRYFAH 534
Qy 301 SRMLVKNKSIWKGKGLVTCRVVHEALPG---SRTLEKS 334
Db 535 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 571

RESULT 7
Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 67.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TONSIL;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR InterPro; IPR003599; IG_c1.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR0033006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_5.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 4; Length 613;
Best Local Similarity 31.2%; Pred. No. 4.3e-37;
Matches 105; Conservative 73; Mismatches 13; Indels 25; Gaps 10;
```

```
Qy 17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPPAKVHVTVLWDQGEAEN 69
Db 241 PLPVIAELPPKVSVF---VPPRDGFFGNPKRS-KLICQATGFSPPQIQVSWLREGQVGS 296
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRRCS 123
Db 297 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 354
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 355 PQDQTAIRVFAIPSPFASIFLTSTLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 414
Qy 184 KHHATTTSITSLPVDADKWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 415 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALHRPVDYLLP 474
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Qy 243 PSPETG---TTRTVTCLIRGFPSEISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 475 PAREQLNRESATITCLVTGFSFADVFQWMQRGOPLSPEKYVTSAPMPPEQAPGRYFAH 534
Qy 301 SRMLVKNKSIWKGKGLVTCRVVHEALPG---SRTLEKS 334
Db 535 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 571

RESULT 8
Q96GA6
ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (protein for MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-CELL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_5.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;
```

```
Query Match 26.3%; Score 488.5; DB 4; Length 614;
Best Local Similarity 31.2%; Pred. No. 4.3e-37;
Matches 105; Conservative 73; Mismatches 13; Indels 25; Gaps 10;
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```
Qy 17 PVTII---PPTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPPAKVHVTVLWDQGEAEN 69
Db 241 PLPVIAELPPKVSVF---VPPRDGFFGNPKRS-KLICQATGFSPPQIQVSWLREGQVGS 297
Qy 70 LPFYTT-----RPKREGGQTFSLQSEVNITQGWMSNTYTHVHNGSIP-EDSSRRCS 123
Db 298 --GVTTDQVQAEAKESGPTTYKVTSLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 355
Qy 124 DDEPRGVITYLPPSPDLIYENGTPKLTCLVLDLSEENITVTVWRERKKSIGSASQST 183
Db 356 PQDQTAIRVFAIPSPFASIFLTSTLTIKESDWLSQSMFTCRVDHRLGTLTFOQNASSMCV 415
Qy 184 KHHATTTSITSLPVDADKWIEGEGYQCRVDHPHPPKPIVRSITKLPGRKL-APEVYMLP 242
Db 416 SHPNATFSAVGEASICEDDWSNGERFTCTVTHDLPSPKQTIISRPKGVALHRPVDYLLP 475
Qy 243 PSPETG---TTRTVTCLIRGFPSEISVQWLNNEDHTGHTTTRPKQKHGTDPSFFLY 300
Db 476 PAREQLNRESATITCLVTGFSFADVFQWMQRGOPLSPEKYVTSAPMPPEQAPGRYFAH 535
Qy 301 SRMLVKNKSIWKGKGLVTCRVVHEALPG---SRTLEKS 334
Db 536 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 572

RESULT 9
Q96AA6
ID Q96AA6 PRELIMINARY; PRT; 618 AA.
AC Q96AA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
```


Db 249 PNVVVF---VPRDGFSGPAPKSKLICEATNFTPKPIITVSLKDKLVESGFTTDPVTI 305
Qy 76 RPREGGQTFSLQSEVNITQGWMSNTYCHVKNGSIF-EDSRRCSDDDEPRVITVL 134
Db 306 ENKGSTPQTKYKISTITISEIDWLNVTCDVRHGLTFLKNVSTCAAS9PSTDLIFT 365
Qy 135 IPPSPDLIYENCTPKLTCLVLDSEENITVWVRKKSGSASQSRSTKHHHTSITS 194
Db 366 IPPSPADIFLSKANLTCVLSNLTATYTNISWASQSGEPLTKIKIMESHNGFTSAK 425
Qy 195 ILPVDKADWIEGQCRVDHDPFKPIVRSITKLPKG--RLAPVYVMLPPSPETG--T 250
Db 426 VASVCVEDNNRKEFVCTVTHRDLSPQKFKSK-PNEVHKHPPAVALLPPAREQLNRE 484
Qy 251 TRVTCLIRGFVPSISVQWLNNEDHTGHHHTTRPKQKHGTDPSFFLYSRMLVKNYSIW 310
Db 485 SATVTCVKGFSADISVQWLQGLPQEKYVTSAPMPGAPGFYFTHSILITVTEB 544
Qy 311 EKNLVTCTVWHEALP---GSRTELS 334
Db 545 NSGETYTCVWGHEALPHLVTERIVDKS 571

RESULT 12
Q8TC63
ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 52.0 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 24.5%; Score 455; DB 4; Length 473;
Best Local Similarity 33.4%; Pred. No. 4.2e-34;
Matches 115; Conservative 67; Mismatches 128; Indels 34; Gaps 12;

Qy 18 VTIIPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVDGQEAENL 70
Db 142 VSVSPASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVTVSNWNGALTSG---VHT 198
Qy 71 PFTYTRPKREGQTFSLQSEVNITQGWMSNTYCHVKNGSIFEDSRRCSDDDEP--- 127
Db 199 FPAVL---QSSGLSLSSVTVFPSS-LGTQTYICNVDHKSNTKVDKRVESKYGPPCP 253
Qy 128 -----RGVITYLIPSPDL-LYENGTPKLTCLVLDSESE-NITVTVWRKKSGS 177
Db 254 SCPAPEFLGGPSVFLPPPKDITMISRTPEVTCVVVDVSDPEQVFNWYVDGVEVHNA 313
Qy 178 ASQRTSKHHHTSITSILPVDKADWIEGQCRVDHDPFKPIVRSITKLPKRLAPE 237
Db 314 KTKPREQNSTYRVVSVLTVLHQDLNKGKCYKCKVSNKGLPSSIEKTLISKAKGQPREPQ 373
Qy 238 VYMLPPSPPEE-TGTRTTRVTCIRGFYPSISVQWLNNEDHTGHHHTTRPKQKHGTDPS 296
Db 374 VTLPSPSEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPEN-NYKTTTPVLD--SDGS 429
Qy 297 PFLYSRMLVKNYSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340
Db 430 FFXSRLTVDKSRWQGNVFCVSNVHEALHNYHT-QKSLSLSIG 472

RESULT 13
Q8TC77
ID Q8TC77 PRELIMINARY; PRT; 471 AA.
AC Q8TC77;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 51.8 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024289; AAH24289.1; -
KW Hypothetical protein.
SQ SEQUENCE 471 AA; 51791 MW; 3887F4CF588660E CRC64;

Query Match 23.8%; Score 441.5; DB 4; Length 471;
Best Local Similarity 31.7%; Pred. No. 7.6e-33;
Matches 110; Conservative 73; Mismatches 127; Indels 37; Gaps 13;
Qy 18 VTIIPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW---LVDGQEAENL 70
Db 137 VTVSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSG---VHT 193
Qy 71 PFTYTRPKREGQTFSLQSEVNITQGWMSNTYCHVKNGSIFE-----DSSR 120
Db 194 FPAVL---QSSGLSLSSVTVFPSS-LGTQTYICNVHKNPSNTKVDKRVESKCDKTH 248
Qy 121 RC-----SDDEPRGVITYLIPSPDL-LYENGTPKLTCLVLDSESE-NITVTVWRKKKS 174
Db 249 TCPPCAPELGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEV 308
Qy 175 IGSASQRTSKHHHTSITSILPVDKADWIEGQCRVDHDPFKPIVRSITKLPKRL 234
Db 309 HNAKTKPREQNSTYRVVSVLTVLHQDLNKGKCYKCKVSNKALPAPIEKTISKAKGQPR 368
Qy 235 APEVYMLPPSPPEE-TGTRTTRVTCIRGFYPSISVQWLNNEDHTGHHHTTRPKQKHG 293
Db 369 EPQYITLPSPDELTKNQVSLTCLVKGFYPSDIAVWESNGQPEN-NYKTTTPVLD--S 424
Qy 294 DPFYFLYSRMLVKNYSIWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340
Db 425 DGSFFLYSKLTVDKSRWQGNVFCVSNVHEALHNYHT-QKSLSLSIPG 470

RESULT 14
Q9RI14
ID Q9RI14 PRELIMINARY; PRT; 437 AA.
AC Q9RI14;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -
DR HSSP; P01842; 7FAB.
MGD; MGI:96446; Igh-4.

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DR InterPro; IPR003600; Ig_like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; Ig_Like; 2.  
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.  
FT NON_TER 437 437 1  
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;  
  
Query Match 23.4%; Score 435; DB 11; Length 437;  
Best Local Similarity 31.2%; Pred. No. 2.8e-32;  
Matches 109; Conservative 66; Mismatches 134; Indels 40; Gaps 13;  
  
Qy 16 GPVTII-----PPTVKLFHSSCDPRGDAHSTTQLLCLVSGFSPAKVHVTW-----LVD 63  
Db 104 GPGTLVTSAAKTTPSV--YPLAPGSAQAQNSMTLGLVKVGYFPEPTVTWNSGSLSS 161  
  
Qy 64 QEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIF----- 115  
Db 162 Q---VHTFPAVLQ-----SDLYTLSSSVTPSSTW-PSETVTCNVAHPASSTKVDKIVP 212  
  
Qy 116 -EDSSRRCSDDPRGVITYLPPSPLD-LYENGTPKLTCLVLDLSEER-NITVTWVRERK 172  
Db 213 RDGCKPCICTVPEVSSVFIFPPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFDDV 272  
  
Qy 173 KSIGASQRSTKHHATTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRK 232  
Db 273 EVHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKRCVNSAAPPAPIEKTIKTGR 332  
  
Qy 233 RLAEVYMLPPSPETGTTR-TVTCLIRGFYPSIISVQWLPNNEEDHTGHHTTTRPKQKH 291  
Db 333 PKAPQVYTIPTPPKEQMAKDVKSLTCMTDFFPEDITVEQWNGQP--AENYKNTQPIMD- 389  
  
Qy 292 GTDPSFFLYSRMLNKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340  
Db 390 -TDGSFYFYSKLNQKSNWEAGNTFTCSVLHEGLHNHHT-EKSLSHSPG 436  
  
RESULT 15  
Q99LC4 PRELIMINARY; PRT; 463 AA.  
AC Q99LC4  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Similar to RIKEN cDNA 1810060009 gene.  
GN IGH-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strauberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003435; AA03435.1; -  
DR HSSP; P01842; 7FAB  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig.cl.  
DR InterPro; IPR003600; Ig_Like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 2.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; Ig_Like; 1.  
DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.  
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
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Query Match 23.4%; Score 434.5; DB 11; Length 463;  
Best Local Similarity 31.6%; Pred. No. 3.4e-32;  
Matches 110; Conservative 65; Mismatches 136; Indels 37; Gaps 13;  
  
Qy 9 TSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLLCLVSGFSPAKVHVTW-----LYDG 64  
Db 136 TVSAAKTTPPSVYP----LAPGSA---AQTNSMTLGLVKVGYFPEPTVTWNSGSLSSG 188  
  
Qy 65 QEAENLFPYTRPKREGGQTFSLQSEVNIITQGMSSNTYTCHVKHNGSIF----- 115  
Db 189 ---VHTFPAVLQ-----SDLYTLSSSVTPSSTW-PSETVTCNVAHPASSTKVDKIVP 239  
  
Qy 116 EDSSRRCSDDPRGVITYLPPSPLD-LYENGTPKLTCLVLDLSEER-NITVTWVRERK 173  
Db 240 DCGCKPCICTVPEVSSVFIFPPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFDDVE 299  
  
Qy 174 SIGASQRSTKHHATTITSILPVDADKWIEGEGYQCRVDHPHPKPIVRSITKLPGRK 233  
Db 300 VHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKRCVNSAAPPAPIEKTIKTGR 359  
  
Qy 234 RLAEVYMLPPSPETGTTR-TVTCLIRGFYPSIISVQWLPNNEEDHTGHHTTTRPKQKH 292  
Db 360 KAPQVYTIPTPPKEQMAKDVKSLTCMTDFFPEDITVEQWNGQP--AENYKNTQPIMD-- 415  
  
Qy 293 TDPSEFFLYSRMLNKSWEKGNLVTCTRVVHEALPGSRTLEKSLHYSAG 340  
Db 416 TDGSFYFYSKLNQKSNWEAGNTFTCSVLHEGLHNHHT-EKSLSHSPG 462  
  
Search completed: March 8, 2003, 07:49:25  
Job time : 35 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 8, 2003, 07:43:50 ; Search time 13 Seconds
(without alignments)
1087.956 Million cell updates/sec

Title: US-09-401-636-4

Perfect score: 1858

Sequence: 1 EFHHHHHTLSLPESGPVTI.....HEALPGSRTLEKSLHVSAGN 341

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1051	56.6	429	1 EPC_RAT	P01855 rattus norv
2	940.5	50.6	421	1 EPC_MOUSE	P06336 mus musculus
3	745	40.1	428	1 EPC_HUMAN	P01854 homo sapien
4	499	26.9	454	1 MUC_HUMAN	P01871 homo sapien
5	490	26.4	479	1 MUCM_RABIT	P04221 oryctolagus
6	488	26.3	458	1 MUC_RABIT	P03988 oryctolagus
7	484.5	26.1	391	1 MUCB_HUMAN	P04220 homo sapien
8	468	25.2	326	1 GC2_HUMAN	P01859 homo sapien
9	464.5	25.0	450	1 MUC_CANFA	P01874 canis fami
10	455.5	24.5	455	1 MUC_MOUSE	P01872 mus musculus
11	455.5	24.5	476	1 MUCM_MOUSE	P01873 mus musculus
12	451.5	24.3	327	1 GC4_HUMAN	P01861 homo sapien
13	449.5	24.2	457	1 MUC_SUNMU	P02768 suncus muri
14	440.5	23.7	330	1 GC1_HUMAN	P01857 homo sapien
15	433.5	23.3	454	1 MUC_MESAU	P06337 mesocricetu
16	426	22.9	322	1 GCA_RAT	P02760 rattus norv
17	424.5	22.8	329	1 GCC_RAT	P02762 rattus norv
18	424.5	22.8	335	1 GCAB_MOUSE	P01864 mus musculus
19	423	22.8	326	1 GC1_RAT	P02759 rattus norv
20	422	22.7	323	1 GC_RABIT	P01870 oryctolagus
21	419	22.6	329	1 GC2_CAVPO	P01862 cavia porce
22	410	22.1	324	1 GC1_MOUSE	P01868 mus musculus
23	410	22.1	393	1 GC1M_MOUSE	P01869 mus musculus
24	408.5	22.0	329	1 GC3_MOUSE	P22436 mus musculus
25	405	21.8	336	1 GC3_MOUSE	P01865 mus musculus
26	405	21.8	405	1 GCB_MOUSE	P01867 mus musculus
27	403.5	21.7	398	1 GC3M_MOUSE	P03987 mus musculus
28	394	21.2	330	1 GC3A_MOUSE	P01863 mus musculus
29	394	21.2	399	1 GCAM_MOUSE	P01865 mus musculus
30	386	20.8	290	1 GC3_HUMAN	P01860 homo sapien
31	386	20.8	438	1 HVC2_HETFR	P23085 heterodontu
32	381.5	20.5	333	1 GCB_RAT	P02761 rattus norv
33	373	20.1	438	1 HVCS_HETFR	P23087 heterodontu

RESULT 1

EPC_RAT ID_EPC_RAT STANDARD; PRT; 429 AA.

AC P01855;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 19 epsilon chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).

RC STRAIN=LOU/C/WSL;

RX MEDLINE=83064537; PubMed=6292865;

RA Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;

RT "Structure and evolution of the heavy chain from rat immunoglobulin

E.";

RL Nucleic Acids Res. 10:6041-6049(1982).

RN [2]

RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).

RX MEDLINE=83182019; PubMed=6820340;

RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;

RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:

construction, identification, and DNA sequence.";

RL DNA 1:335-343(1982).

RN [3]

RP SEQUENCE OF 205-306 FROM N.A.

RX MEDLINE=82174576; PubMed=6803238;

RA Hellman L., Pettersson U., Bennich H.;

RT "Characterization and molecular cloning of the mRNA for the heavy

(epsilon) chain of rat immunoglobulin E.";

Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).

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CC -----

CC EMBL; J00744; AAA41379.1; ALT INIT.

DR PIR; A02143; EHRT.

DR HSHP; P01854; 1IGE.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig_ci.

DR InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00410; IG_Like; 3.

DR SMART; SM00407; IGG1; 1.

DR PROSITE; PS00290; IG_MHC; 3.

DR Immunoglobulin domain; Immunoglobulin C region.

KW NON_TER

FT CONFLICT 168 168 R -> N (IN REF. 2).

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FT CONFLICT 308 308 P -> L (IN REF. 2).
SQ SEQUENCE 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;

Query Match 56.6%; Score 1051; DB 1; Length 429;
Best Local Similarity 62.6%; Pred. No. 3.3e-72;
Matches 206; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 17 PVTIIPPTVKLFHSSCDPRGDASHITQLLCLVSGSPAKVHVTVLVDGQEAENLFPYTTR 76
Db 97 PYNITKPTVDLLHSSCDPNA-FHSTIQLYCFYVYGHQNDVSIHLMDDRKI-----YETH 150
Qy 77 PK-----REGGQFSLQSEVNIQGGWMSNTYTCHVKGNSIFEDSSRCSDDPRGVIT 132
Db 151 AQNVLIKEGKLASYSLRNITQQQWMSSTFTCKVTSQGENYWAHTRCSDDEPRGVIT 210
Qy 133 YLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIGSASQSTKHHATTSI 192
Db 211 YLIPSPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIGSASQSTKHHATTSI 270
Qy 193 TSILPVDAKDWTEGEGYQCRVDHPHPPKDIVRSITKLPKRLAPEVYMLPPSPETGTTR 252
Db 271 TSILPVDAKDWTEGEGYQCRVDHPHPPKDIVRSITKLPKRLAPEVYMLPPSPETGTTR 330
Qy 253 TVTCLIRGYPSEISVQWLPNNEEDHTGHTTTRPKOHGTDPSPFLYSRMLVNSKIWEK 312
Db 331 TLTCLIQNFPPEDISVQWLDKSLPKSOHSITTPUKYNGSNQRPFIISRLVTKALWTQ 390
Qy 313 GNLVTCRVVHEALPGSRTEKLSLHYSAGN 341
Db 391 TKQFTCRVTHEALREPRKLTERTISLGN 419

RESULT 2
EPC_MOUSE
ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P06336; P01856;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236092; PubMed=6329728;
RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:
RT comparison with the human epsilon gene sequence.";
RL EMBO J. 1:1117-1123(1982).
RN [2]
RP REVISIONS.
RA Honjo T.;
RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 34-421 FROM N.A.
RX MEDLINE=83117774; PubMed=6818553;
RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon
RT chain cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).

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CC -----
DR EMBL; X01857; CAA25977.1; -.
DR EMBL; X01857; X01857; Muridae; Murinae; Mus.
DR EMBL; X01857; X01857; Muridae; Murinae; Mus.
```

```
DR PIR; A02145; EHMSS.
DR PIR; A02144; EHMSS.
DR HSP; P01854; ILGE.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; Ig_like; 2.
DR SMART; SM00407; IGCL; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DOMAIN 1 90 CH1.
FT DOMAIN 91 197 CH2.
FT DOMAIN 198 304 CH3.
FT DOMAIN 305 421 CH4.
FT DISULFID 23 75 BY SIMILARITY.
FT DISULFID 121 180 BY SIMILARITY.
FT DISULFID 226 285 BY SIMILARITY.
FT DISULFID 330 392 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F3A06B47 CRC64;

Query Match 50.6%; Score 940.5; DB 1; Length 421;
Best Local Similarity 55.2%; Pred. No. 6.9e-64;
Matches 191; Conservative 46; Mismatches 100; Indels 9; Gaps 5;

Qy 2 FHHHHHTLSLPES-----GPVTIIPPTVKLFHSSCDPRGDASHITQLLCLVSGSPAKV 56
Db 73 FTCHVTHPPSFNESTRILVRPNVITEPLELHSSCDPNA-FHSTIQLYCFYGHILNDV 131
Qy 57 HVTWLVGQEAENLFPYTTRPKRGQGTFSLOSEVNIQGGWMSNTYTCHVKGNSIFE 116
Db 132 SVSWLMDRETTDTLAQTALVLIKEE-GKLASTCSKLNITEQQWMSSTFTCKVTSQVDYL 190
Qy 117 DSSRCSDDPRGVITVLIPEPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIG 176
Db 191 AHTRCRCPDHEPRGVITVLIPEPDLVYENGTPKLTCLVLDLESENIITVWVRERKKSIG 249
Qy 177 SASQSTKHH-HATTSTISILPVDAKDWIEGEGYQCRVDHPHPPKPIVRSITKLPKRLA 235
Db 250 SASQWYTKHNNATTSITSLPVAKDWIEGEGYQCRVDHPHPPKPIVRSITKLPKRLA 309
Qy 236 PEVYMLPPSPETGTTRVTCVIRGYPSEISVQWLPNNEEDHTGHTTTRPKOHGTDP 295
Db 310 PEVYVFPPEESEDKRTLTCLIQNFPPEDISVQWLDGKLSNSQHSSTTTPLKSGNSQ 369
Qy 296 SFFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRTEKLSLHYSAGN 341
Db 370 GFFIFSRLEVAKTLWTKQKQFTCVIHEALQKPRKLEKTISTSLGN 415

RESULT 3
EPC_HUMAN
ID EPC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ig epsilon chain C region.
GN IGHE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```


RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).

RN [3].

RP REVISIONS (GAL).

RX MEDLINE=81066716; PubMed=6777162;

RA Mihaesco E., Barnikol-Watanabe S., Barnikol H.U., Mihaesco C.,

RA Hilschmann N.,

RT "The primary structure of the constant part of mu-chain-disease

RT protein BOT";

RL Eur. J. Biochem. 111:275-286(1980).

RN [4]

RP SEQUENCE (WALDENSTROM'S OU), DISULFIDE BONDS, AND CARBOHYDRATES.

RX MEDLINE=74005511; PubMed=4742735;

RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.,

RT "Complete amino acid sequence of the mu heavy chain of a human IgM

RT immunoglobulin";

RL Science 182:287-291(1973).

RN [5]

RP PARTIAL SEQUENCE FROM N.A.

RX MEDLINE=82059479; PubMed=6795593;

RA Rabbitts T.H., Forster A., Milstein C.P.;

RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of

RT C mu, C delta and C gamma genes and associated switch sequences.";

RL Nucleic Acids Res. 9:4509-4524(1981).

RN [6]

RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.

RX MEDLINE=81077306; PubMed=677778;

RA Dolby T.W., Devuono J., Croce C.M.;

RT "Cloning and partial nucleotide sequence of human immunoglobulin mu

RT chain cDNA from B cells and mouse-human hybridomas";

RL Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).

CC -!- MISCELLANEOUS: ALL 4 COMBINATIONS OF THE S/G & V/G POLYMORPHISMS

CC AT POSITIONS 192 AND 216 HAVE BEEN OBSERVED IN HUMAN MU CHAINS.

CC -----

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CC -----

DR EMBL; X17115; CAA34971.1; ALT SEQ.

DR EMBL; X57086; -; NOT_ANNOTATED_CDS.

DR PIR; A02162; MHU.

DR HSSP; P01857; 1FC1.

DR Genew; HGNC:5541; IGMM.

DR MIM; 147020; -.

DR GlycoSuiteDB; P01871; -.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00410; Ig_like; 1.

DR SMART; SM00407; IGc1; 3.

DR PROSITE; PS00290; IG MHC; 3.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

FT NON_TER 1 1

FT DOMAIN 1 105

FT DOMAIN 106 218

FT DOMAIN 219 324

FT DOMAIN 325 454

FT DISULFID 14 14

FT DISULFID 28 98

FT DISULFID 135 198

FT DISULFID 215 215

FT DISULFID 245 304

FT DISULFID 292 292

FT INTERCHAIN (WITH A LIGHT CHAIN).

FT INTERCHAIN (WITH A HEAVY CHAIN).

FT INTERCHAIN (WITH A HEAVY CHAIN IN ANOTHER

FT OF THE 5 TETRAMERIC SUBUNITS OF THE

FT MOLECULE).

FT DISULFID 352 414

FT DISULFID 453 453

FT CARBOHYD 46 46

FT CARBOHYD 210 210

FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .).

FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).

FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .).

FT VARIANT 192 192 /FTID=CAR_000219.

FT VARIANT 216 216 S -> G.

FT VARIANT 216 216 /FTID=VAR_003903.

FT VARIANT 216 216 V -> G.

FT VARIANT 216 216 /FTID=VAR_003904.

SQ SEQUENCE 454 AA; 49556 MW; 21EC72EADC56922E CRC64;

Query Match 26.9%; Score 499; DB 1; Length 454;

Best Local Similarity 31.5%; Pred. No. 1.5e-30;

Matches 106; Conservative 72; Mismatches 135; Indels 24; Gaps 9;

Qy 17 PVTII---PPVKLFHSCDPR----GDAHSTIQLCLVSGFSPAKVHVTVLWVQAEAN 69

Db 102 PLPVIAELPPKVSF---VPPRDGFFGNPRSKSLICATQGSFPRQIQVSLREGQVGS 158

Qy 70 LFPYTT----RPKREGQTFSLQSEVNIQTQGMSSNTYTCVKGHSIF-EDSSRCS 123

Db 159 --GVTTQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTRVDHRLGLTQQNASSMCV 216

Qy 124 DDEPRGVITYLIPSPDLVYENGPKLTCLVLDLSEENITVTWVRKKSIGSASQST 183

Db 217 PDQDTAIRVFAIPPSFASIFLTSTKLTCLVTLDTVDSVTISWTRONGEAVKTHNISE 276

Qy 184 KHHATTSITSLIPVDADKWIEGEGYQCRVDHPFPRIVRSITKLPKRL-APENVMLP 242

Db 277 SHPNATFSVAGEASICEDDMNSGERFCTVTHTDLPSPKQTSIRPKGVALLHRPDVYLLP 336

Qy 243 PSPETG--TTRVTCLIRGYPSEISVOWLPNNEEDHTGHTTTRPKQDHTGDPSPFLY 300

Db 337 PARQLNRESATITCLVTGSPADVFQVMQORGLSPKQVTSAPNPEQAPGRYFAH 396

Qy 301 SRMLVNKSIMWKGMLVTCRVVHEALPG---SRTLEKS 334

Db 397 SILTVSEEMWTGTYTCVVAHEALPNRVTERTVDKS 433

RESULT 5

MUCM RABIT STANDARD; PRT; 479 AA.

ID MUCM RABIT

AC P04221;

DT 20-MAR-1987 (Rel. 04, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig mu chain C region membrane-bound form.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A. (A2 ALLOTYPED).

RX MEDLINE=84088930; PubMed=6418803;

RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;

RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain

RT of VHA2 allotype: comparisons with VHA1 and membrane mu sequences.";

RL J. Immunol. 132:490-495(1984).

CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES

CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.

CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-

CC TERMINAL SEGMENTS.

CC -----

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CC -----

DR EMBL; K01357; AAA31293.1; -.

DR PIR; A02165; MHRBM.

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DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON TER 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT TRANSEM 459 476 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 249 308 BY SIMILARITY.
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 356 418 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 479 AA; 52351 MW; 689C637A7B19FC CRC64;

Query Match 26.4%; Score 490; DB 1; Length 479;
Best Local Similarity 32.4%; Pred. No. 7.7e-30;
Matches 114; Conservative 62; Mismatches 150; Indels 18; Gaps 8;

Qy 5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDP-RGDAHSTIQLCLVSGFSPAKVHTWLV 62
Db 94 HSNRNRLRVSPFVDSLPNNVSPFIPPRDSFGSGTRKSLICQATGSPKQISVWLR 153

Qy 63 DQQAEN---LFPYTRPRKREGGQTFSLQSEVNIITQGWMSNTYTCVKGNGSIFEDS- 118
Db 154 DQKVESGLVKPVEAETKGAGPATFSISSMLTITSDWLSQSLYTCRVDHGRGIFDKV 213

Qy 119 ---SRCSDDPERGVITYLIPSPDLVNGTPKLCLVLDLESENITVWVRKKSIG 176
Db 214 SMSSECSSTPSPGIQVFFIAPSFADTFLSKSARLCLVTLDTLTYSGLNISWASHNGKALD 273

Qy 177 SASQBSTKHHTATTSITSLPVDADKWIAGEGYQCRVDHPHPKPIVRSITKLPKRLA- 235
Db 274 THMNITESHPNATFSAMGEASVCAEDWESGEOFTCTVTHADLPFLKHTISK--SREVAK 331

Qy 236 --PEVYMLPPSPPEE--TGTRTVCILRGFVPSISVQWLPNNEDHTGHTTTTRPQKH 291
Db 332 HPPAVYVLPAREQLVRESATVCLVGFSPADVFVQVQQRQGLSSDKYTSAPAPEP 391

Qy 292 GTDPFFLYSLRMVNKSWEKGNLTCRVVHEALP---GSRITLEKSLHYSAG 340
Db 392 QAPGLYFTHSTLITVEDWNSGETTCVVGHEALPHMVTERTVDKSTGEVG 443

RESULT 6
MUC_RABIT
ID_MUC_RABIT STANDARD; PRT; 458 AA.
AC P03988;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_taxid=9986;
RN [1]

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RP SEQUENCE FROM N.A. (A2 ALLOTYPED).
RX MEDLINE=84089930; PubMed=6418803;
RA Bernstein K.B., Alexander C.B., Reddy E.P., Mage R.G.;
RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain
RL J. Immunol. 132:490-495(1984).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; K01357; -; NOT_ANNOTATED_CDS.
CC PIR; A02164; MHRB.
CC HSSP; P01842; 7FAB.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_c1.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 4.
CC SMART; SM00410; IG like; 2.
CC SMART; SM00407; IGL; 2.
CC PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON TER 1
FT DOMAIN 1 106 CH1.
FT DOMAIN 107 222 CH2.
FT DOMAIN 223 327 CH3.
FT DOMAIN 328 458 CH4.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 90 BY SIMILARITY.
FT DISULFID 137 200 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 219 219 BY SIMILARITY.
FT DISULFID 249 308 BY SIMILARITY.
FT DISULFID 296 296 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 356 418 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 284 284 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 458 AA; 49897 MW; F338D6A3B28E4864 CRC64;

Query Match 26.3%; Score 488; DB 1; Length 458;
Best Local Similarity 32.7%; Pred. No. 1e-29;
Matches 114; Conservative 62; Mismatches 149; Indels 24; Gaps 9;

Qy 5 HHHHTLSLPESGPV-TIIPPTVKLFHSSCDP---GDAHSTIQLCLVSGFSPAKVHT 59
Db 94 HSNRNRLRVSPFVDSLPNNVSPF---IPRDSFGSGTRKSLICQATGSPKQISV 150

Qy 60 WLVDQQAEN---LFPYTRPRKREGGQTFSLQSEVNIITQGWMSNTYTCVKGNGSIFE 116
Db 151 WLRDQKVESGLVKPVEAETKGAGPATFSISSMLTITSDWLSQSLYTCRVDHGRGIFD 210

Qy 117 DS---SRCSDDPERGVITYLIPSPDLVNGTPKLCLVLDLESENITVWVRK 173
Db 211 KVSMSSECSSTPSPGIQVFFIAPSFADTFLSKSARLCLVTLDTLTYSGLNISWASHNGK 270

Qy 174 SIGSQBSTKHHTATTSITSLPVDADKWIAGEGYQCRVDHPHPKPIVRSITKLPKGR 233
Db 271 ALDTHMNITESHPNATFSAMGEASVCAEDWESGEOFTCTVTHADLPFLKHTISK--SRE 328

Qy 234 LA---PEVYMLPPSPPEE--TGTRTVCILRGFVPSISVQWLPNNEDHTGHTTTTRPQ 288

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RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A02148; G2HU.
DR HSP; P01857; 1FC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IG1; 2.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 17 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match 25.2%; Score 468; DB 1; Length 326;
Best Local Similarity 34.4%; Pred. No. 2.28-28;
Matches 111; Conservative 66; Mismatches 116; Indels 30; Gaps 12;
Qy 35 RGDASHSTQLLCVSGFSPAKVHVTTW----LVDGQAEHLFPYTRPRKREGQTSLOSE 90
Db 16 RSTSESTAALGCLVKDYFPEPTVSNWNSGALTSG---VHTPAVL-----QSSGLYSLSV 68
Qy 91 VNITGQMMSNNTYCHVKH---NGSIFEDSSRRCSDDP-----RGVITYLIPPSPL 140
Db 69 VTPVSSNF-GTQTYTCNVDHKPSNTKVDKTVKCCVCPAPPVAGPSVFLFPKPK 127
Qy 141 D-LYENGTPKLTCLVLDSESE-NITVTWVRKKKISGASORSTKHHHTTSITSLPV 198
Db 128 DTLMSIRTFEPTCVVVDVSHEDPEVFQNMVYDGVVHNAKTPREEQFNSTFRVVSILT 187
Qy 199 DAKWIEGEGQCRVDHPFKPIVRSITKLPGLKLAPEVYMLPSPBE-TGTTTIVTCL 257
Db 188 VHQDWLNKEVYKCKVSNKGLFAPIEKTSIKYQGPREFQVYTLPPSREMTKNQVSLCL 247
Qy 258 IRGFYPSISQVQLPNNBEDHTGHHHTTPQKDHGCTDPSFFLYSRMLVKNKSIWEKGNLVT 317
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Db 248 VKGYFSPSDIAVEWSSNGOPEN--NYKTPPMLD--SDGSFFLYSKLTVDKRWQGNVFS 303
Qy 318 CRVVHEALPGSRTLEKSLHYSAG 340
Db 304 CSVMHEALHNHYT-QKSLSLSPG 325
RESULT 9
MUC_CANFA
ID MUC_CANFA STANDARD; PRT; 450 AA.
AC P01874; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE OF 1-177 (MOO).
RX MEDLINE=80077682; PubMed=117299;
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
RP SEQUENCE OF 178-450 (MOO).
RX MEDLINE=78180587; PubMed=653360;
RA Wasserman R.L., Capra J.D.;
RT "Amino acid sequence of the Fc region of a canine immunoglobulin M:
RT interspecies homology for the IgM class.";
RL Science 200:1159-1161(1978).
DR PIR; A02169; MHDG.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00410; IG like; 2.
DR SMART; SM00407; IG1; 2.
DR PROSITE; PS00290; Ig_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER 1
FT SEQUENCE 450 AA; 48895 MW; 9D460DA9D1012F5D CRC64;
Query Match 25.0%; Score 464.5; DB 1; Length 450;
Best Local Similarity 31.8%; Pred. No. 6e-28;
Matches 109; Conservative 69; Mismatches 136; Indels 29; Gaps 12;
Qy 10 LSLPE--SGPVTIPTTVKLFHSSCDPRGDAHSTTLCLVSGFSPAKVHVTTW-LVDGQE 66
Db 106 LTLPEVSG---FIPPRDAFFG---BPRKS-----QLICQASGFSPQV---WSLRDGKQ 151
Qy 67 AENLFPPYTT-----RPRKREGQTSLOSEVNITQGMSSNTYTCVHKNGSIF-EDSSR 120
Db 152 IES--GVTTNEVZAKZSGPTTYKVTSMLTIQEDAWLSQSFTCKVHRGLTFQONASS 209
Qy 121 RCDDEPRGVITYLIPPSPLDIYENGTPKLTCLVLDSESENIITVWVRKKKISGASQ 180
Db 210 MCTSDQPVGISIFTIPPSFASIFNTKSAKSLCLVTLATYDSVTISWTREENGALKHTN 269
Qy 181 RSTKHHHTTITSITLPVDADKDWTEGEGYQCRVDHPHPKPIVRSITKLPGLKRL-APEVY 239
Db 270 ISEHPNGTTFAMGEATVCVEWESGEQFTCTVHTDLPVLKQTIISRPKGVAVHMPSVY 329
Qy 240 MLPPSPETG--TTRTVCILIRGFYPSISQVQLPNNBEDHTGHHHTTRPQKHGTDPSF 297
Db 330 VLPPSREQLDLRESATLSCLVTGYSPDPVFQVQWKGQVPPDSVYTSAPMPEQPAPGLY 389
Qy 298 FLYSRMLVKNKSIWEKGNLVTCTRVHREALPGSRTLEKSLHYSAG 340
Db 390 FAHSILTYSSEENAGETTYTCVAHESLP-NRVTERSVDKSTG 431
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RESULT 10
MUC MOUSE
ID MUC MOUSE STANDARD; PRT; 455 AA.
AC P01872;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076590; PubMed=6255422;
RA Kawakami T., Takahashi N., Honjo T.;
RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and
RT comparison with other immunoglobulin heavy chain genes.";
RL Nucleic Acids Res. 8:3933-3945(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82051295; PubMed=6795090;
RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;
RT "Sequence of the gene for the constant region of the mu chain of
RT Balb/c mouse immunoglobulin.";
RL Gene 15:33-42(1981).
RN [3]
RP SEQUENCE FROM N.A. (MYELOMA TPC183).
RX MEDLINE=81165562; PubMed=6260591;
RA Auffray C., Rougeon F.;
RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu
RT chain of mouse immunoglobulin.";
RL Gene 12:77-86(1980).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).
RX MEDLINE=79223904; PubMed=111247;
RA Kehry M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;
RT "Amino acid sequence of a mouse immunoglobulin mu chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979).
RN [5]
RP REVISION (MOPC 104E).
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V00827; -, NOT_ANNOTATED_CDS.
CC PIR; A02166; MHMS.
CC HSSP; P01857; 1FC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_C1.
CC InterPro; IPR003600; Ig_Like.
CC Pfam; PF00047; Ig; 4.
CC SMART; SM00410; Ig_Like; 2.
CC SMART; SM00407; IGC1; 2.
CC PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Alternative splicing.
KW NON_TER 1
KW DOMAIN 106
KW DOMAIN 217
KW DOMAIN 218
KW DOMAIN 324
KW DOMAIN 325
KW DOMAIN 436
KW DOMAIN 437
KW DOMAIN 455
KW DISULFID 14
KW DISULFID 14
KW DISULFID 28
KW DISULFID 89
KW DISULFID 136
KW DISULFID 199
KW DISULFID 216
KW DISULFID 216
KW DISULFID 246
KW DISULFID 305
KW DISULFID 293
KW DISULFID 293
KW DISULFID 353
KW DISULFID 415
KW DISULFID 454
KW DISULFID 454
KW CARBOHYD 46
KW CARBOHYD 46
KW CARBOHYD 211
KW CARBOHYD 211
KW CARBOHYD 243
KW CARBOHYD 243
KW CARBOHYD 281
KW CARBOHYD 281
KW CARBOHYD 442
KW CARBOHYD 442
KW VARIANT 78
KW VARIANT 78
KW VARIANT 101
KW VARIANT 101
KW VARIANT 226
KW VARIANT 226
KW VARIANT 258
KW VARIANT 258
KW VARIANT 258
KW VARIANT 258
KW VARIANT 368
KW VARIANT 368
KW SEQUENCE 455 AA; 50101 MW; 4CB57CB602F9B51 CRC64;

Query Match 24.5%; Score 455.5; DB 1; Length 455;
Best Local Similarity 32.1%; Pred. No. 2.9e-27;
Matches 105; Conservative 63; Mismatches 140; Indels 19; Gaps 8;

Qy 23 PTVKLFHSSCDPR---GDAHSTTQLCLVSGSPAKVHVTVLVDGQEAENLF---PVT 75
Db 112 PNVNVP---VPRDGFSGPAPRKSLICEATNFTPKPTVSWLKDGLVESGFTDPVTI 168
Qy 76 RPKREGGOTFSLQSEVNITQGMSSNTYTCVHKHNGSIF-EDSSRRCSDDPRGVITVL 134
Db 169 ENKSGTPTQYKIVSTLTISEIDWLNLVNVTQVDRHGUTFLKNWSSTCAASPSTDLIFT 228
Qy 135 IPPSPDLIYENGTPKLTCLVLDLSEENITVTVRERKKSIGSASQSRSTKHHHTSITS 194
Db 229 IPPSPADIFLSKANLTCLVSNLATYETLNISWASQSGEPLTKIKIMESHPPNGTFSAGK 288
Qy 195 ILPVADKDWIEGEGVQCHVDHPHPKPIVRSITKLPK--RLAPEVYMLPPSPETG--T 250
Db 289 VASVCVEDMNNRKEFVCTVTHRDLPSPQKFTISK-PNEVHKHPPAVYLLPPAREQLNRE 347
Qy 251 TRVTCLIRGVFVPEISVQWLPNNEEDHTGHTTTPKQDHDGTDPSFFLYSRMLVKNKSIW 310
Db 348 SATVTCLVKGFSPADISVQWLQRGQLLPQEKVYTSAPMPPEGAPGFYTHSILTVTESEW 407
Qy 311 EKGNLVTCRVVHEALP---GSRITLES 334
Db 408 NSGETYTCVVGHEALPHLVLTERTVDKS 434

RESULT 11
MUC MOUSE
ID MUC MOUSE STANDARD; PRT; 476 AA.
AC P01873;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 433-476 FROM N.A.
RX MEDLINE=80222874; PubMed=6771020;
RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R.,
```

RA Hood L.;
RT "Two mRNAs can be produced from a single immunoglobulin mu gene by
RN alternative RNA processing pathways."
RL Cell 20:313-319(1980).
RN [2]
RP SEQUENCE OF 410-476 FROM N.A. (MYELOMA MOPC 104E).
RX MEDLINE=8022873; PubMed=6771019;
RA Rogers J., Early P., Carter C., Calame K., Bond M., Hood L.,
RA Wall R.;
RT "Two mRNAs with different 3' ends encode membrane-bound and secreted
RN forms of immunoglobulin mu chain."
RL Cell 20:303-312(1980).
CC -!- ALTERNATIVE PRODUCTS: DURING DIFFERENTIATION, B LYMPHOCYTES
CC SWITCH FROM EXPRESSION OF MEMBRANE-BOUND IGM TO SECRETION OF IGM.
CC THE MU CHAINS OF MEMBRANE AND SECRETED IGM DIFFER IN THEIR C-
CC TERMINAL SEGMENTS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-409 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00821; CAA24202.1; ;
DR PIR; A02167; MHMSM.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGH4.
DR PROSITE; PS00290; Ig_MHC; 3.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 217 CH2.
FT DOMAIN 218 324 CH3.
FT DOMAIN 325 436 CH4.
FT TRANSMEM 456 473 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 28 89 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 136 199 BY SIMILARITY.
FT DISULFID 216 216 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 246 305 BY SIMILARITY.
FT DISULFID 293 293 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 353 415 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 476 AA; 52656 MW; 8D476575A5204071 CRC64;

Query Match 24.5%; Score 455.5; DB 1; Length 476;
Best Local Similarity 32.1%; Pred. No. 3.1e-27;
Matches 105; Conservative 63; Mismatches 140; Indels 19; Gaps 8;
Oy 23 PTVKLFHSSCDPR----GDAHSTIQLCLVSGFSPAKVHTVWLVDGQEAENLF---PYVT 75
Db 112 PNVVVF---VPRDGFSGPAPRKSCLKIENFTPKPTVSVLWKGKLVESGFTDPTVI 168
Oy 76 RPKRGGQTFSQSEVNTIQGQMSNTVTHVKNNGSIF-EDSSRRCCDDPRGVITVL 134
Db 169 ENKGSTPTQYKVIISTLTISEIDWLNLVYTCRVDHRLTFLKNVSTCAASPSDILFT 228
Oy 135 IPPSPDLVYENCTPKLCLVLDESENTVTVWRKKSIGSASQRTKHHHTSITS 194
Db 229 IPPSPADIFLSKANLTCLVSNLATYETLNISWASQSGEPLETKIKIMESHFNGTFSAGK 288

Oy 195 ILPVDADKWIEBEGYQCRVDHPHPKPIVRISITKLPKGK--RLAPEVYMLPPSPBETG--T 250
Db 289 VASVCVEDNNRKEFVCTVTRDLPSPOKPFISK-PNEVHKHPPAVYLLPPAREQLNLR 347
Oy 251 TRVTCTLRGYPSEISVQWLPNNEEDHTGHTTTRPKDCHGTDPSFFLYSRMLYKSTW 310
Db 348 SATVTCLVKGFSPADISVQWLQGLLPQEKYVTSAPMPEGAPGFYFTHSILTVTEBEM 407
Oy 311 EKGNLVTCRVVHEALP---GSRITLEKS 334
Db 408 NSGETYTCVVGHEALPHLVTVTERTVDKS 434
RESULT 12
ID GC4 HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1996 (Rel. 01, Last sequence update).
DT 21-JUL-1996 (Rel. 01, Last sequence update).
DT 16-OCT-2001 (Rel. 40, Last annotation update).
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene."
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.B., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain."
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; ;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGH4.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 247 305

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SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 24.3%; Score 451.5; DB 1; Length 327;
Best Local Similarity 34.3%; Pred. No. 3.9e-27;
Matches 111; Conservative 62; Mismatches 120; Indels 31; Gaps 11;

QY 35 RGDASTIQLCLVSGFSPAKVHVW---LVDGQEAENLPYTRPKREGQTSLOSE 90
Db 16 RSTSSAALGCLVXDYPPEVTVSNWNGALTSG---VHTFPAVL-----QSSGLYLSV 68

QY 91 VNITQGMSSNTYCHVKHNGSIFEDSSRRCSDDPE-----RGVITYLIPSP 139
Db 69 VTVPESS-LGTXTYICNDVHKSNKVDKVESKYGCPSPCAPPEFLGGPSVFLFPPKP 127

QY 140 LD-LVENGTPKLTCLVLDLESE-NITVWVRKKSIGSASQRTKHHTATSTISILP 197
Db 128 KDTLMISRTPEVTCVVDVSDPEQVFNWYVDGVEVHNKTKPREQFNSTYRVSVLT 187

QY 198 VDAKMWIEGEGYQCRVDHPFPKPIVRSITKLPKRLAPEVVMPLPSPPE-TGTTTRVTC 256
Db 188 VLHQDLNGKEYKCKVSNKGLPSSLEKTSKAKGQRPQVTLPPSOEMTKNQVSLTC 247

QY 257 LIRGYPSEISVQWLPNNBEDTGHHTTRPKQDHTGTPSPFELYSRMLVKNKSIWEKGNLV 316
Db 248 LVKGYPSDIAVEWESNGOPEN--NYKTTTPVLD--SDGSFELYSLTLVDKSRWQEGNVF 303

QY 317 TCRVVEALPGSRITLKSLSHYAG 340
Db 304 SCVNMHEALHNYT-QKSLSLSLG 326

RESULT 13
MUC SUNMU STANDARD; PRT; 457 AA.
AC P20768;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu chain C region.
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.
OX NCBI_TaxID=9378;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89232144; PubMed=2497033;
RA Ishiguro H., Ichihara Y., Namikawa T., Nagatsu T., Kurosawa Y.;
RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and
comparison with mouse and human mu genes.";
RL FEBS Lett. 247:317-322(1989).

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EMBL; X13920; CAA32113.1; ALT_INIT.
DR PIR; S03961; S03961.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig like; 1.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00290; IG MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 105
FT DOMAIN* 1 105 CH1.
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FT DOMAIN 106 220 CH2.
FT DOMAIN 221 326 CH3.
FT DOMAIN 327 457 CH4.
FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 27 89 BY SIMILARITY.
FT DISULFID 136 200 BY SIMILARITY.
FT DISULFID 217 217 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 248 307 BY SIMILARITY.
FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 355 417 BY SIMILARITY.
FT DISULFID 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 56074 MW; 56C8C086DA4462E9 CRC64;

Query Match 24.2%; Score 449.5; DB 1; Length 457;
Best Local Similarity 29.9%; Pred. No. 8.3e-27;
Matches 100; Conservative 76; Mismatches 138; Indels 21; Gaps 8;

QY 21 IPTVTKLPHSSCDPR---GDAHSTIQLCLVSGFSPAKVHVTVLVDGQEAENLPYTT- 75
Db 110 LPPNVISF---VPRNPSFGNHPRTSQLICQASGSPRTIVMSWLQRCPEVPQPSLVSTSA 166

QY 76 ---RPKREGQTSLQSEVNITQGMSSNTYTCHVKHNGSIFED---SSRRCSDDEPRGV 130
Db 167 VEAPKPGSGPTTFRVISRLTITENELWSQREFTQALHKGLTKQNVSSVCWGDSTGTGI 226

QY 131 IYLIPLSPDLIYENGTPKLTCLVLDLESEENITVWVRKKSIGSASQRTKHHTATT 190
Db 227 SVFLLPPTFANIFLTQSAQLTCLVTGLATYDLSIDMSRQNGEALQTHVNISESHPNSTF 286

QY 191 SITSLIPVDKADWIEGEGYQCRVDHPFPKPIVRSITKLPKRLA---PEVVMPLPSPPEE 247
Db 287 TAKGHASVCREWESGKFTCTVQHSIDLPSLKQSLSR--PKVDANDPPSVFLVPPAQEQ 344

QY 248 --TGTRTVTCLIRGFYPSSEISVQWLPNNEDHTGHHTTTPKQKHGTDPSFFLYSRMLV 305
Db 345 LKLRESASITCLVDFSPDPVDFVQWQHGGQVPDPKHYYTSNPTPEPQNPGLYFVHSILTV 404

QY 306 NKSTWEKGNLVTQVVEHALPGSRITLKSLSHYAG 340
Db 405 SEKDWSSGESFSCVVGHEALPLSVT-EKAVDKTSG 438

RESULT 14
GCL_HUMAN STANDARD; PRT; 330 AA.
ID GCL_HUMAN
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2];
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=3489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
```


Db 58 --QSSGLYSLSSVTVTPSS--LGTYICNVNHNKPSNTKVDKKVEPKSCDKTHTTCCPCA 114
Qy 124 DDEPRGVITYLPPSPDL-LYNGTPKTLCLVLESEB-NITVTWVRERKKSIGASQR 181
Db 115 PELLGPGSVFLPPPKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKP 174
Qy 182 SPKHHHTTSITSLPVDADKIEGEGYOCYCRVDHPPKPIVRSITKLPGLAPEVYML 241
Db 175 REEQNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAGQPRFPQVYL 234
Qy 242 PPSPEE-TGTTTRVTCLIRGFYPSISVQWLPNNBEDHTGHHTTTRPOKHGTDPSFFLY 300
Db 235 PSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPEN--NYKTTTPVLD--SDGSFFLY 290
Qy 301 SRMLVNSIWEKGNLVTCTRVHPEALPGSRTELSLHYSAG 340
Db 291 SKLTVDKSRWQGNVFCVSMVEALHNYHT-QKSLSLSPG 329

RESULT 15
MUC_MESAU
ID MUC_MESAU STANDARD; PRT; 454 AA.
AC P06337;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig mu chain C region.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297761; PubMed=2994005;
RA McGuire K.L., Duncan W.R., Tucker P.W.;
RT "Phylogenetic conservation of immunoglobulin heavy chains: direct
RL comparison of hamster and mouse Cmu genes."
RC Nucleic Acids Res. 13:5611-5628(1985).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X02804; CAA26574.1; -.
DR PIR; A02168; MHHY.
DR HSSP; P01854; LIGE.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00410; Ig_Like; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 218 CH2.
FT DOMAIN 219 324 CH3.
FT DOMAIN 325 454 CH4.
FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 27 88 BY SIMILARITY.
FT DISULFID 135 198 BY SIMILARITY.
FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 245 304 BY SIMILARITY.
FT DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 352 414 BY SIMILARITY.
FT DISULFID 453 453 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 45 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;
Query Match 23.3%; Score 433.5; DB 1; Length 454;
Best Local Similarity 30.7%; Pred. No. 1.3e-25;
Matches 106; Conservative 68; Mismatches 154; Indels 17; Gaps 9;
Qy 5 HHHT---LSLPESGPTIIPPTVKLFHSSCDP-RGDAHSTIQLCLVSGSPAKVHVTV 60
Db 91 HGNNTKDLRVP-IPVVTMNPVSVFVPSRDAPSGPAPKRSRLFCFASNFSPKQITVSW 149
Qy 61 LVDGQEAENLF---PYTRPKREGGQTFPSLOSEVNIITOGMMSSNTYTCHVKHNGSIF-E 116
Db 150 LRDKFPVKSGETTEPVPEDRGSGPRYKVIKSTLTITSDMLNLSVYTCRVDHRLGTLFWK 209
Qy 117 DSRRCSDDEPRGVITYLPPSPDLVYNGTPKTLCLVLDSEBENITVTWVRERKKSIG 176
Db 210 NVSSTCAASPTDIOAFPIPPSFVGIFFLNKSAITLCLVTNLATYDTLNISSWSRSGEPLE 269
Qy 177 SASQSTKHHTTTSITSLPVDADKIEGEGYOCYCRVDHPPKPIVRSITKLPCK--RL 234
Db 270 TKTKLTESHHPNGTFSAGEANVCVEDMDSDGKEFVCTVTHRDLPSPQKPFISK-PRMNKT 328
Qy 235 APEVYMLPPSPPEE--TGTRTCTVCLIRGFYPSISVQWLPNNBEDHTGHHTTTRPOKHG 292
Db 329 PPAYVQQLAREQILRESAVTCLVKGFSFADIFVQWLQRGQPLSQDKYVTSAPMREPQ 388
Qy 293 TDPGFLLYSRMLVNKSIWEKGNLVTCTRVHPEALP---GSRTELEKS 334
Db 389 APHLVFTHSVLTVEEWNSETVTCVVGHEALPHMVTERTVDRS 433

Search completed: March 8, 2003, 07:48:38
Job time : 14 secs